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FJ194029.1	344973	15286.2	12478.4	18207.9	16749.3	14720.7	14133.0
GQ095772.1	459901	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ093131.1	420434	22453.4	23492.5	18916.2	17279.2	23678.7	19821.8
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GQ024872.1	484802	9079.9	9511.6	15777.3	10405.2	8129.3	8069.5
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GQ098074.1	378595	9010.6	10068.2	13056.9	12894.1	11188.9	9006.1
GQ038697.1	468566	6386.7	3393.1	8370.1	6654.9	4234.9	7020.2
GQ103037.1	423661	13725.7	14057.6	11458.2	12001.1	14065.5	7209.9
GQ110989.1	426707	15276.5	18293.2	5883.6	4849.3	2917.7	5780.8
GQ107352.1	457872	9916.9	10468.4	11012.8	10224.7	14546.7	11760.7
GQ099559.1	462883	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ103975.1	388693	16823.2	18124.9	16188.4	17486.4	12428.5	19153.1
GQ107827.1	375294	14925.3	16655.6	17704.6	12628.4	17712.5	13467.5
GQ101255.1	392813	9217.8	9403.8	10830.6	10370.1	9787.8	7780.5
GQ098240.1	435539	14614.5	11665.0	16420.4	15401.6	10314.1	12691.3
GQ113214.1	406645	20479.1	17491.8	20397.2	18620.7	18799.1	16127.9
GQ112960.1	439333	10028.0	8406.2	2337.2	13699.0	15220.1	12824.4
GQ104366.1	419585	7827.4	3261.0	8757.3	10355.3	6104.7	4475.0
GQ101732.1	389090	3331.8	5643.9	7054.2	6747.5	10735.5	16713.5
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GQ097026.1	412407	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
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GU208284.1 gg_id:547389 Study on Sediment Dongping Lake sediment clone Ftb1-13
GQ076015.1 gg_id:401721 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw7
GQ102667.1 gg_id:423993 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw6
GQ086253.1 gg_id:380973 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ076360.1 gg_id:464830 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
GQ093338.1 gg_id:426669 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
GQ096276.1 gg_id:392445 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ095778.1 gg_id:461247 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ106715.1 gg_id:430703 Topographical and Temporal Human Skin Microbiome skin back clone nbw539g04c1
GQ107078.1 gg_id:400296 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw544d0
GQ092132.1 gg_id:408192 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw406d10c
GQ074925.1 gg_id:394487 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ095280.1 gg_id:439776 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ116205.1 gg_id:446613 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw689b07
GQ114443.1 gg_id:378277 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw6
GQ098886.1 gg_id:463306 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558c
GQ083326.1 gg_id:435413 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ114781.1 gg_id:394344 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ098192.1 gg_id:392840 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ084693.1 gg_id:393141 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26
GQ108256.1 gg_id:410573 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw604d08c
GQ102757.1 gg_id:421042 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw6
GQ072733.1 gg_id:378255 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw20
GQ039081.1 gg_id:375242 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu524f04
GQ114889.1 gg_id:445841 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ076201.1 gg_id:391413 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
GQ075048.1 gg_id:411252 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ083240.1 gg_id:376150 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ105046.1 gg_id:459679 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ106378.1 gg_id:402127 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ104300.1 gg_id:392896 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU137341.1 gg_id:275823 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
GQ101124.1 gg_id:422851 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
GQ085321.1 gg_id:376597 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273h08c
GQ091385.1 gg_id:413382 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw345d0
GQ099474.1 gg_id:440159 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
GQ085395.1 gg_id:444162 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw275b05c
GQ105693.1 gg_id:464415 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ107726.1 gg_id:458060 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw553c03
GQ111845.1 gg_id:403180 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw

GU208284.1	547389	5186.1	5573.5	14429.3	7433.0	4386.5	3919.1
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GQ102667.1	423993	15607.5	14266.1	22952.8	17415.3	9434.5	11577.0
GQ086253.1	380973	10169.3	9986.6	12699.8	9332.7	10026.1	9160.5
GQ076360.1	464830	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ093338.1	426669	8829.2	10477.7	10292.0	10864.5	14275.8	10555.5
GQ096276.1	392445	12579.4	10772.4	14570.2	14556.2	8216.5	11271.8
GQ095778.1	461247	14218.4	8251.2	19348.4	15838.2	10919.2	13590.9
GQ106715.1	430703	10226.0	10202.1	12548.2	11914.3	11938.1	11512.3
GQ107078.1	400296	20418.0	16977.4	20506.5	18849.0	17497.6	17370.1
GQ092132.1	408192	175.7	401.3	232.0	509.2	179.9	140.6
GQ074925.1	394487	9003.9	5039.2	13629.2	8625.8	6531.9	6543.0
GQ095280.1	439776	17973.0	13427.0	10711.6	19480.7	18377.5	15308.3
GQ116205.1	446613	24295.4	23599.6	18976.4	14069.8	22816.0	20566.4
GQ114443.1	378277	19121.5	15643.0	11936.5	19547.5	16869.5	17566.3
GQ098886.1	463306	13693.1	9487.5	19559.7	14372.1	10297.1	11130.7
GQ083326.1	435413	11391.5	10810.9	15830.4	12024.7	13802.6	11402.8
GQ114781.1	394344	13068.0	12080.2	11480.5	12564.8	13811.4	10633.1
GQ098192.1	392840	11454.4	6916.8	11653.8	12306.3	5329.7	10003.2
GQ084693.1	393141	23738.7	25741.0	14622.0	16930.5	17988.1	16417.4
GQ108256.1	410573	19462.2	20341.1	14311.1	15118.1	24522.6	18587.3
GQ102757.1	421042	20892.1	18635.7	11838.6	20309.6	23634.6	18908.2
GQ072733.1	378255	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ039081.1	375242	9362.4	5632.7	6765.1	12091.0	7188.7	8691.0
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GQ076201.1	391413	18160.0	14745.2	10564.3	18442.9	7844.9	11310.4
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GQ083240.1	376150	9635.2	7815.8	3884.3	11720.7	14734.3	14035.9
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GQ105046.1	459679	17417.6	10778.4	16629.4	17024.0	11090.3	11378.9
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GQ104300.1	392896	14769.1	15051.6	16701.5	11750.7	14442.7	13131.2
EU137341.1	275823	23418.7	16619.7	33147.2	25362.6	18463.4	19160.9
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GQ085321.1	376597	18576.0	16512.5	12273.6	19488.0	25856.9	22117.3
GQ091385.1	413382	15578.7	11944.9	17853.7	13931.5	12342.2	12477.8
GQ099474.1	440159	11270.8	8714.1	11284.4	11952.4	5208.3	7636.7
GQ085395.1	444162	27137.3	26957.2	18519.0	19595.4	26117.8	23842.2
GQ105693.1	464415	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ107726.1	458060	14261.7	13793.1	13622.5	12825.1	12011.2	11879.3
GQ111845.1	403180	8904.4	9767.3	10923.1	15821.2	11417.2	9706.7

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GQ104862.1 gg_id:385489 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ094189.1 gg_id:413699 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw371
GQ098315.1 gg_id:444176 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ095353.1 gg_id:384663 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ092809.1 gg_id:461022 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ104646.1 gg_id:381018 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ111155.1 gg_id:467858 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ106732.1 gg_id:410395 Topographical and Temporal Human Skin Microbiome skin back clone nbw540a08c1
GQ103906.1 gg_id:405375 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ092477.1 gg_id:381489 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ098533.1 gg_id:411808 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw703c
AF035054.1 gg_id:7154 Aquabacterium commune str. B8
GQ092791.1 gg_id:432096 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ074158.1 gg_id:399701 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ093926.1 gg_id:465715 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ094903.1 gg_id:422518 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ075450.1 gg_id:392786 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ106160.1 gg_id:440227 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ112615.1 gg_id:425450 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw675a0
GQ087936.1 gg_id:401130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw360f05
GQ096656.1 gg_id:405212 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ104884.1 gg_id:409812 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ098793.1 gg_id:374865 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw702f
GQ111479.1 gg_id:374805 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw668d0
GQ083195.1 gg_id:418155 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ094917.1 gg_id:390509 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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GQ098315.1	444176	11382.1	7728.0	29074.0	11548.1	10518.7	7100.9
GQ095353.1	384663	10908.9	12344.7	21941.7	14875.9	22475.5	18912.1
GQ092809.1	461022	9976.5	8307.3	6097.9	14587.1	5546.6	9806.4
GQ104646.1	381018	4539.6	6823.1	5422.3	12924.9	4469.1	4687.7
GQ111155.1	467858	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ106732.1	410395	7580.4	9427.2	13009.7	9795.6	14380.8	10704.2
GQ103906.1	405375	13983.8	11747.4	17142.0	17211.8	9576.9	7029.9
GQ092477.1	381489	9418.1	7722.3	9387.2	15037.2	9177.7	10872.4
GQ098533.1	411808	8160.0	9275.0	13150.4	8116.8	10978.8	8937.6
AF035054.1	7154	4901.2	5987.0	17715.8	7026.2	5595.3	7104.3
GQ092791.1	432096	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
GQ074158.1	399701	10778.3	10058.5	11922.2	11374.2	14372.9	10790.6
GQ093926.1	465715	3294.8	4464.5	13470.8	5461.4	4213.2	3514.3
GQ094903.1	422518	12752.0	14156.8	14132.0	10727.0	13267.3	11648.1
GQ088805.1	416059	6708.1	5966.4	10632.8	7607.5	6606.0	6017.4
GQ096931.1	439045	7840.4	8017.7	12626.3	10538.8	10798.7	8807.8
GQ115493.1	382820	19972.6	19801.1	13031.7	16890.8	21006.9	17547.3
GQ086509.1	449715	27137.3	26957.2	18519.0	19595.4	26117.8	23842.2
GQ096963.1	386705	24151.7	24428.8	12428.8	17064.8	25790.7	22331.8
GQ098857.1	376357	4550.5	4933.2	10550.2	6793.1	6448.8	3846.0
GQ115467.1	420921	33814.6	19664.7	14452.1	17849.5	22902.2	19138.3
GQ092665.1	446463	9726.6	7951.5	12928.8	10582.2	5965.3	6486.8
GQ095303.1	437043	19120.3	12641.5	28554.1	20828.8	16075.6	19770.9
GQ098365.1	382539	12401.2	13650.4	13511.7	10860.0	14821.7	11149.6
GQ075450.1	392786	13475.0	11542.3	12475.6	16577.7	14462.7	16227.2
GQ106508.1	416642	8071.6	9018.9	9489.6	7579.0	5214.1	5219.0
GQ102214.1	439491	33814.6	19664.7	14452.1	17849.5	22902.2	19138.3
GQ103880.1	386947	9926.0	7480.7	7809.2	12310.3	4347.9	4782.1
GQ087469.1	382165	12518.0	5881.3	19183.3	14509.6	8463.3	9800.3
GQ099577.1	385972	8703.8	8129.8	9058.0	9793.0	6071.6	6947.0
GQ106160.1	440227	8396.2	8454.0	11362.8	9772.4	10221.3	8696.2
GQ112615.1	425450	5887.2	8187.4	14127.0	12440.1	9405.0	5292.1
GQ087936.1	401130	13401.8	5547.8	16948.5	14533.1	7715.9	9231.7
GQ096656.1	405212	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
GQ104884.1	409812	4121.7	4009.6	3958.8	6280.2	5414.1	5208.0
GQ098793.1	374865	9765.3	6096.4	6589.9	10639.2	4756.0	9188.0
GQ111479.1	374805	15423.6	13244.4	7522.7	17772.2	16212.8	17566.7
GQ083195.1	418155	11834.2	15328.1	17891.8	13468.3	15303.7	13325.6
GQ094917.1	390509	18660.6	14244.0	18749.8	18162.9	12632.6	14237.3

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GQ090667.1 gg_id:405518 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ083039.1 gg_id:390142 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ098162.1 gg_id:380146 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
DQ256338.1 gg_id:143054 subsurface water clone EV818BHEB5102502DRLWq27f093
GQ073341.1 gg_id:417934 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h05c
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GQ102169.1	428134	23738.7	25741.0	14622.0	16930.5	17988.1	16417.4
GQ096441.1	442199	17593.4	16705.7	21791.5	16028.5	18456.8	15264.5
GQ086073.1	427140	21527.2	7646.1	21895.1	16454.7	4779.2	7948.5
GQ107250.1	455909	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ099382.1	412852	8518.9	5966.8	7312.4	13152.0	5855.3	9678.7
GQ108042.1	416785	11191.4	12193.9	10348.5	11423.6	14609.3	12343.7
GQ102237.1	400564	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
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GQ074951.1	379845	7827.4	3261.0	8757.3	10355.3	6104.7	4475.0
GQ101681.1	409736	19665.3	15753.4	13155.2	21659.3	21750.3	18272.5
GQ096799.1	387658	7858.3	5607.3	7295.5	8244.6	4530.4	5681.4
GQ106313.1	434645	16110.6	13856.8	20380.3	17176.4	9929.1	12112.6
GQ098454.1	416052	13336.1	13162.5	12960.7	13633.4	13471.4	13056.5
GQ107437.1	388677	8954.1	6167.3	10058.7	10804.4	3576.2	6336.6
GQ072027.1	425451	15604.7	16342.6	21790.1	15120.0	15300.4	14448.4
GQ101769.1	446314	13240.9	10669.1	6833.7	11841.8	5284.7	8405.6
GQ106772.1	395615	9332.1	8603.2	14945.3	9874.6	8885.2	9261.2
GQ102792.1	428990	33814.6	19664.7	14452.1	17849.5	22902.2	19138.3
GQ105662.1	443364	10822.7	6849.5	15894.3	11734.9	6238.7	6338.1
GQ092840.1	449677	14910.6	16014.1	14284.2	13629.0	16136.7	13518.6
GQ102631.1	409965	6960.5	8750.0	11964.2	8400.9	12250.7	7581.8
GQ090667.1	405518	15340.0	17474.1	16137.9	13462.9	17942.7	14714.6
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GQ075486.1	439302	9319.8	8078.7	11059.7	13070.9	7476.8	6081.2
GQ099604.1	460359	16018.7	16547.6	18063.9	12682.5	17465.9	11419.1
GQ102871.1	398359	10862.0	12007.2	13690.8	10372.1	14017.7	10384.1
GQ096999.1	437352	14151.8	14309.8	5974.4	15071.8	21600.0	17281.6
GQ070431.1	408351	3470.5	3455.3	3640.7	8443.9	757.3	6710.8
GQ096449.1	442302	8929.0	3088.8	4041.7	12879.8	1325.7	3305.3
GQ098162.1	380146	7713.3	9885.3	14115.8	9878.1	12598.0	9903.9
DQ256338.1	143054	14435.8	12859.5	23116.6	14937.7	14954.4	12921.1
GQ073341.1	417934	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ089284.1	397167	2760.0	4862.9	8444.2	4068.0	1412.0	2410.3

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GQ099399.1 gg_id:419335 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
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GQ102260.1 gg_id:450738 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ104271.1 gg_id:421128 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ097409.1 gg_id:423333 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ103140.1 gg_id:425963 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ104570.1 gg_id:408674 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ114678.1 gg_id:446944 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ098799.1 gg_id:463680 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw702f
GQ095346.1 gg_id:466437 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ098614.1 gg_id:438874 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw704c
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GQ104325.1 gg_id:435282 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ098626.1 gg_id:395482 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw704e
GQ065835.1 gg_id:410251 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw93e08
GQ002442.1 gg_id:507220 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ100937.1 gg_id:407376 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ102857.1 gg_id:443360 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ105112.1 gg_id:434680 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ111638.1 gg_id:389727 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ094483.1 gg_id:450005 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ085363.1 gg_id:385711 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw274e08
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GQ083324.1 gg_id:381611 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ096548.1 gg_id:396128 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw389e0
GQ088502.1 gg_id:400498 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ085429.1 gg_id:393065 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw275e12
GQ093244.1 gg_id:422046 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
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GQ105445.1 gg_id:414232 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ083319.1 gg_id:418267 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ114235.1 gg_id:409114 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
GQ094988.1 gg_id:397716 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ105166.1 gg_id:419019 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ085299.1 gg_id:403315 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273f05c
GQ075442.1 gg_id:401247 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

GQ110914.1	423841	12338.1	10187.1	14555.8	15733.4	3918.1	5681.9
GQ098768.1	456497	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
GQ097495.1	413580	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ099399.1	419335	20892.1	18635.7	11838.6	20309.6	23634.6	18908.2
GQ088950.1	423637	8912.4	4961.1	8923.5	13880.6	3883.4	5391.7
GQ087783.1	435728	15079.4	7928.8	16779.9	17015.6	7741.7	9415.5
GQ102260.1	450738	11148.2	7496.0	15738.6	10175.4	5668.9	6883.4
GQ104271.1	421128	13058.0	8792.6	10725.9	16241.9	6479.2	8639.3
GQ097409.1	423333	10768.2	8552.9	10966.4	11931.5	8907.4	8703.0
GQ103140.1	425963	16608.6	19099.5	16894.0	15889.9	14242.3	13621.1
GQ104570.1	408674	1272.8	2823.9	11872.9	2712.4	2915.1	2615.0
GQ114678.1	446944	14759.1	12306.3	14400.3	17398.1	13243.9	14869.4
GQ098799.1	463680	11136.2	7851.0	13134.3	10758.3	4129.2	7734.8
GQ095346.1	466437	8743.9	9251.1	8676.9	11248.7	15976.8	13661.8
GQ098614.1	438874	10638.1	10417.7	16119.4	11779.7	9205.0	8932.0
GQ113677.1	419303	8659.7	9386.4	15487.8	8184.9	8839.1	7991.2
GQ092976.1	410213	21190.6	21925.3	10376.8	15765.0	14178.1	11880.8
GQ104325.1	435282	24558.8	22420.7	22100.3	19466.5	25450.2	24572.7
GQ098626.1	395482	23117.0	22728.9	21325.6	19183.9	21789.8	18591.7
GQ065835.1	410251	27397.3	25922.6	15785.3	20880.3	26127.2	23212.4
GQ002442.1	507220	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ100937.1	407376	18276.8	13832.6	21090.3	17573.7	15009.4	17254.6
GQ102857.1	443360	12332.7	10678.2	11466.1	17748.6	3113.9	8879.6
GQ105112.1	434680	12518.0	5881.3	19183.3	14509.6	8463.3	9800.3
GQ111638.1	389727	9920.9	11472.6	10917.5	7658.1	5384.8	8685.8
GQ094483.1	450005	18449.9	19405.4	16866.4	18135.4	26695.3	22146.6
GQ085363.1	385711	2025.0	1492.0	2487.9	4384.6	1201.7	1705.5
GQ093177.1	413380	15615.9	13164.2	8686.2	16819.0	19576.9	18754.4
GQ083324.1	381611	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ096548.1	396128	15298.3	14315.1	11522.6	21149.9	16640.3	15830.3
GQ088502.1	400498	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ085429.1	393065	10789.4	9088.9	14204.5	12949.7	7788.2	8045.0
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GQ114235.1	409114	15021.2	11384.5	13153.1	15711.3	10145.8	12933.9
GQ094988.1	397716	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ105166.1	419019	20837.5	17548.9	21120.5	19811.3	20872.3	16826.9
GQ085299.1	403315	9929.8	6779.1	10551.6	11899.6	4742.9	5817.2
GQ075442.1	401247	15276.5	18293.2	5883.6	4849.3	2917.7	5780.8

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GQ096984.1 gg_id:456391 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw392c04
GQ087633.1 gg_id:395170 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ089274.1 gg_id:403270 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
GQ102983.1 gg_id:412025 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ106180.1 gg_id:414005 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ105862.1 gg_id:400055 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw.
GQ111088.1 gg_id:405408 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ096715.1 gg_id:465697 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ116368.1 gg_id:385029 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692b03
GQ090547.1 gg_id:401567 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ110601.1 gg_id:456043 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ112382.1 gg_id:460510 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ115541.1 gg_id:457193 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687c03
GQ086751.1 gg_id:442310 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw348g08
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GQ111326.1 gg_id:374536 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw665d0
GQ082990.1 gg_id:384388 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ104723.1 gg_id:465683 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ093892.1 gg_id:459297 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ092677.1 gg_id:375778 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ107829.1 gg_id:459195 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw554h06
GQ099303.1 gg_id:372704 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ093840.1 gg_id:450052 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ007766.1 gg_id:501899 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1
GQ085575.1 gg_id:467638 Topographical and Temporal Human Skin Microbiome skin palm clone nbw277f12c1
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GQ106226.1 gg_id:410414 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ114989.1 gg_id:442080 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
GQ098615.1 gg_id:399091 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw704c
GQ103013.1 gg_id:411167 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ096433.1 gg_id:454507 Topographical and Temporal Human Skin Microbiome skin back clone nbw388b07c1
GQ063017.1 gg_id:467562 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw96f07c
GQ092966.1 gg_id:452755 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407d06c
GQ105604.1 gg_id:411014 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ097452.1 gg_id:455656 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ098301.1 gg_id:423615 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ098382.1 gg_id:460459 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558h

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GQ087633.1	395170	14162.5	11381.3	9829.7	16307.3	16368.3	14278.7
GQ089274.1	403270	19120.3	12641.5	28554.1	20828.8	16075.6	19770.9
GQ102983.1	412025	6895.8	9431.0	5822.2	8830.9	5356.0	4212.0
GQ106180.1	414005	10639.9	7186.2	13066.0	10484.1	6714.4	8062.7
GQ105862.1	400055	16378.6	17654.8	11787.3	18129.0	19888.1	17257.5
GQ111088.1	405408	15249.8	12838.5	23856.6	15772.2	20474.7	16385.7
GQ096715.1	465697	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ116368.1	385029	13490.3	11167.1	20841.3	13581.7	12368.1	11387.3
GQ090547.1	401567	18496.8	15509.8	20541.8	18031.5	17507.4	13760.5
GQ110601.1	456043	4121.7	4009.6	3958.8	6280.2	5414.1	5208.0
GQ112382.1	460510	8810.4	7336.4	5074.3	12628.1	7025.4	8292.4
GQ115541.1	457193	11859.8	11126.8	6516.2	14025.3	18022.9	15192.5
GQ086751.1	442310	18557.8	11947.0	13855.6	19760.2	6591.4	13353.7
GQ099633.1	449888	3850.8	4042.2	8996.0	10151.3	4545.0	5405.6
GQ114990.1	421031	18651.9	18106.6	17296.5	17829.8	21346.0	18195.8
GQ096193.1	394613	7756.5	9097.7	7089.3	10620.9	13251.8	9828.0
GQ111326.1	374536	8345.0	7722.7	11622.5	11188.4	5584.3	9074.8
GQ082990.1	384388	15251.7	15261.4	16756.4	16273.3	20693.7	16251.4
GQ104723.1	465683	15276.5	18293.2	5883.6	4849.3	2917.7	5780.8
GQ114426.1	450026	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ093892.1	459297	22789.6	20065.8	23917.1	20778.9	22267.3	18413.5
GQ092677.1	375778	28799.4	26846.8	27260.5	23337.2	24970.9	24378.9
GQ107829.1	459195	9982.1	9803.7	11480.0	11882.1	12613.4	8422.0
GQ099303.1	372704	5647.7	5956.4	3093.2	6551.6	173.9	893.5
GQ093840.1	450052	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ007766.1	501899	15916.2	12955.2	9795.1	18320.0	17645.1	15244.7
GQ085575.1	467638	12821.8	6403.4	6081.3	14298.7	1662.6	2318.4
GQ113890.1	384247	15749.0	16190.0	17688.2	16380.6	12680.0	13993.8
GQ106226.1	410414	23028.7	20758.0	17549.6	21676.1	23791.5	19857.5
GQ114989.1	442080	14568.7	10837.1	21709.4	16050.3	10551.1	13390.0
GQ098615.1	399091	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ103013.1	411167	8383.5	9996.7	17787.9	10388.2	13938.4	10862.5
GQ096433.1	454507	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ063017.1	467562	19222.1	17036.7	18412.9	17991.7	16087.8	15526.6
GQ092966.1	452755	0.7	0.7	1.1	0.6	0.6	0.6
GQ105604.1	411014	22223.5	22578.5	22610.6	17051.6	22026.0	19681.4
GQ097452.1	455656	22824.6	23461.4	16911.4	19076.1	22488.5	20375.9
GQ098301.1	423615	13228.9	13459.9	15536.2	13372.8	17305.1	14103.0
GQ098382.1	460459	6629.6	5463.6	8781.6	7168.0	4350.2	5221.0

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GQ098876.1	466920	21726.2	19968.9	14249.8	20468.4	17073.3	16547.1
GQ023641.1	486027	1304.6	2693.3	7071.9	2464.4	2375.2	1489.1
GQ114131.1	444930	16187.1	8500.9	11929.5	16029.7	6350.9	8955.1
GQ104007.1	373241	7513.9	9602.2	7080.1	10565.0	3429.3	4761.1
GQ114890.1	460626	9337.4	4310.7	12785.4	7453.8	7305.1	4543.7
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GQ107356.1	401324	12900.3	16320.2	22112.4	16634.7	14403.9	12366.4
GQ071853.1	460767	8123.3	8206.7	7205.4	10876.4	10746.9	9333.7
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GQ107341.1	463047	8995.4	7571.2	1593.2	12098.9	16495.4	15149.1
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GQ104478.1	386746	14486.0	16508.8	16134.9	12925.1	16579.7	13413.1
GQ085253.1	465225	22995.6	21321.9	24442.0	20651.3	21327.5	19185.6
GQ101888.1	451830	7597.6	7658.0	12910.3	14459.4	8441.4	7158.2
GQ106347.1	408767	9913.2	9463.4	11739.1	10371.7	11200.5	8760.8
GQ085412.1	415306	20311.1	21563.1	15421.1	18020.4	20816.9	19441.1
GQ104422.1	419642	23592.2	25701.4	22860.3	19588.2	24148.6	19824.1
GQ106360.1	373090	5893.5	8397.2	8057.3	8739.4	9736.0	7806.5
GQ101657.1	451658	16147.6	13812.8	15992.5	15146.4	13505.4	12790.1
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GQ105538.1	382009	18176.2	14466.9	15598.1	15122.3	15751.6	15579.8
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GQ076154.1	386432	17340.0	17344.9	14426.1	15660.7	17966.0	15798.0
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GQ090491.1	424751	8125.5	4651.6	6032.1	9683.4	4151.3	6527.4
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GQ096777.1	422605	11840.1	11916.6	5314.2	15791.3	21936.8	18759.0
GQ072007.1	456584	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2

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EU137378.1 gg_id:263071 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
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GQ102998.1 gg_id:465256 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ097621.1 gg_id:423576 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw454c12
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GQ110456.1	377986	20971.7	21555.8	20192.4	19028.6	19490.6	18003.9
GQ097497.1	390727	4569.7	6628.9	11106.5	5341.0	3714.3	4358.0
EU137378.1	263071	18376.6	18005.5	21118.9	18837.3	19098.0	16985.4
GQ106322.1	375416	10181.9	8116.4	9697.2	11201.2	12033.5	11955.1
GQ098148.1	423145	10381.3	9453.0	9400.2	12299.9	13195.7	12138.0
GQ095279.1	373868	0.7	0.7	1.1	0.6	0.6	0.6
GQ106940.1	456878	10208.0	8161.0	9947.3	10285.4	4913.9	5538.7
GQ102859.1	412167	17359.8	12489.9	21422.6	20236.5	13341.0	16313.9
GQ072207.1	391775	7997.3	7838.6	18163.3	26817.3	10278.9	9244.1
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GQ092959.1	418843	14151.8	14309.8	5974.4	15071.8	21600.0	17281.6
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GQ107130.1	457880	9976.5	8307.3	6097.9	14587.1	5546.6	9806.4
GQ105710.1	390950	14289.8	11952.4	5090.5	18427.9	18034.7	15265.0
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GQ093380.1	424051	14568.7	10837.1	21709.4	16050.3	10551.1	13390.0
GQ088030.1	463644	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ096253.1	382616	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
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GQ102864.1	465702	4121.7	4009.6	3958.8	6280.2	5414.1	5208.0
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GQ096522.1 gg_id:398230 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw389c0
AJ239300.1 gg_id:6446 Neisseria cinerea str. F3
FJ387582.1 gg_id:359267 Burkholderia andropogonis str. 6268
FM872738.1 gg_id:367189 occupant source house floor dust clone FB01C03
AY792252.1 gg_id:125947 Humic Lake clone CrystalBog2B1
AY792253.1 gg_id:119501 Humic Lake clone CrystalBog571B4
EU827473.1 gg_id:344718 Burkholderia sp. str. TFD4
FJ796443.1 gg_id:569235 Burkholderia terrae str. IMER-B1-41
Y17009.1 gg_id:7211 Burkholderia caribensis str. MWAP64
Y17011.1 gg_id:7220 Burkholderia caribensis str. MWAP84
AY949189.1 gg_id:131367 Burkholderia hospita A42-8

GQ105020.1	418529	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
GQ092730.1	465508	14568.7	10837.1	21709.4	16050.3	10551.1	13390.0
GQ083122.1	373837	15276.5	18293.2	5883.6	4849.3	2917.7	5780.8
GQ065813.1	456255	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ104925.1	393701	20892.1	18635.7	11838.6	20309.6	23634.6	18908.2
GQ092721.1	391669	22834.6	21703.7	31047.3	20644.1	24968.8	19573.4
GQ114633.1	399871	7650.2	6998.6	12239.1	9021.0	7047.1	7280.1
GQ088511.1	416361	12374.9	7765.7	13446.0	13804.0	6191.8	9034.0
GQ083003.1	446402	9397.5	8773.9	15540.1	9974.5	10200.1	7549.6
GQ107854.1	379213	10028.0	8406.2	2337.2	13699.0	15220.1	12824.4
GQ076369.1	465751	3791.4	4002.9	9926.6	7068.1	2056.4	4638.0
GQ094590.1	423686	4173.3	18847.3	17052.2	20583.9	24330.6	20691.5
GQ074101.1	460377	16450.6	15701.8	14615.7	16099.7	17225.6	16717.7
GQ108196.1	389050	9926.6	11341.0	14090.5	10937.3	12760.2	9892.8
GQ098255.1	391739	19465.1	17059.4	12897.9	18749.2	12867.5	16446.1
GQ102276.1	371860	11431.1	11946.1	13334.9	11492.2	14055.8	9870.3
GQ104369.1	375972	20743.2	17790.5	19510.7	17323.3	17606.9	19493.3
GQ083369.1	438138	12825.0	8576.3	33486.0	12479.7	14495.3	6838.9
GQ094943.1	415506	20479.1	17491.8	20397.2	18620.7	18799.1	16127.9
GQ075561.1	412177	5241.6	6478.9	12181.7	7874.8	5605.2	4648.9
GQ108827.1	400906	12039.2	12461.3	21953.3	12513.5	11978.7	10540.1
GQ092884.1	468541	12311.7	8734.9	22274.6	13982.1	12988.9	12918.3
GQ088292.1	453181	12658.5	9008.1	14661.6	16381.9	8519.8	8561.0
GQ088516.1	383129	775.3	1964.5	4751.3	1592.3	1579.4	1089.5
GQ107631.1	407370	24841.9	24559.1	21511.4	18951.0	23142.6	21606.2
GQ076095.1	383528	17417.6	10778.4	16629.4	17024.0	11090.3	11378.9
GQ038881.1	442518	12440.5	7945.0	11912.9	14134.9	4200.5	8635.4
GQ094960.1	445863	11112.9	12469.9	16018.7	10539.9	9565.6	8123.9
GQ086828.1	458190	13157.5	11574.6	8030.1	14069.3	13637.5	13656.2
GQ104675.1	408705	10537.8	9782.6	3281.2	12447.0	13409.4	12157.1
GQ096522.1	398230	6493.2	7828.2	13469.7	10452.9	9543.1	6395.3
AJ239300.1	6446	11292.0	9857.3	19532.0	16255.2	12965.0	16429.1
FJ387582.1	359267	4054.7	3123.9	8411.4	7062.6	1518.1	3256.5
FM872738.1	367189	5427.6	6803.9	12270.1	8237.5	6257.7	8559.2
AY792252.1	125947	4242.0	6845.3	4536.0	5882.8	4051.7	5322.6
AY792253.1	119501	1617.9	1788.4	1777.4	1410.9	1408.1	1834.5
EU827473.1	344718	1520.7	1390.0	3024.9	2445.4	1340.5	3117.9
FJ796443.1	569235	3568.2	984.9	1747.6	3976.9	339.7	1258.7
Y17009.1	7211	1116.5	1523.9	1908.9	1830.6	1525.3	2248.0
Y17011.1	7220	1517.6	2082.0	3159.2	2802.4	2919.4	4511.8
AY949189.1	131367	5268.3	4331.2	8307.1	10278.6	4755.9	8614.2

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EU024153.1 gg_id:245134 Burkholderia caribensis str. CIP 106784
Y17010.1 gg_id:7219 Burkholderia caribensis str. MWAP71
AY949188.1 gg_id:131028 Burkholderia hospita A57-3
AB091191.1 gg_id:532737 Burkholderia fungorum str. KN-19
GQ181142.1 gg_id:578615 Genetic and vitro evaluation growth-promoting rhizobacteria four native forest spec
AB091187.1 gg_id:591807 Burkholderia fungorum str. TU-138
EU447188.1 gg_id:265915 Burkholderia fungorum str. SW3
AB091185.1 gg_id:556961 Burkholderia fungorum str. TU-97
EU024155.1 gg_id:239548 Burkholderia fungorum str. CIP 107096
AB091190.1 gg_id:565827 Burkholderia fungorum str. KN-17
AB091193.1 gg_id:569412 Burkholderia fungorum str. KN-23
AB091192.1 gg_id:579372 Burkholderia fungorum str. KN-20
EU447189.1 gg_id:266794 Burkholderia fungorum str. SW6
AY568512.2 gg_id:111993 Burkholderia fungorum str. NW-2
AB091181.1 gg_id:584797 Burkholderia fungorum str. ANA-18
AB091189.1 gg_id:570439 Burkholderia fungorum str. KN-08
AB091184.1 gg_id:584364 Burkholderia fungorum str. TU-82
AY178065.1 gg_id:103619 Burkholderia sp. CS2 CS 2
EU024170.1 gg_id:244278 Burkholderia gladioli str. CIP 104582
EU024175.1 gg_id:256228 Burkholderia plantarii str. CIP 105979
AB012916.1 gg_id:34465 Burkholderia gladioli
AY268163.1 gg_id:91595 Burkholderia gladioli str. 2002721590
AY586517.1 gg_id:98973 Burkholderia gladioli str. LUC15
EU024176.1 gg_id:239929 Burkholderia plantarii str. CIP 105769
AY586515.1 gg_id:107629 Burkholderia gladioli str. LUC57
GQ337697.1 gg_id:581096 Burkholderia gladioli str. S9
GQ900610.1 gg_id:537377 Burkholderia gladioli str. A6
AB023646.1 gg_id:7270 Burkholderia gladioli
EU090891.1 gg_id:264212 Burkholderia gladioli str. R1879
AY949201.1 gg_id:134333 Burkholderia pyrrocinia RG6-5
GQ337699.1 gg_id:532689 Burkholderia gladioli str. S1
EU560426.1 gg_id:273601 Burkholderia gladioli str. TNAU-1
EU024168.1 gg_id:252056 Burkholderia gladioli str. CIP 105410
EU053154.1 gg_id:239216 Burkholderia gladioli str. MS102
AY154377.1 gg_id:75813 Burkholderia glathei Hg 17
AJ971354.1 gg_id:138733 Burkholderia sp. str. SB5
AY154368.1 gg_id:75249 Burkholderia glathei Hg 3
AY154378.1 gg_id:76415 Burkholderia glathei Hg 18
AY154367.1 gg_id:77259 Burkholderia glathei Hg 2
AY307365.2 gg_id:137089 Burkholderia sp. str. M12

AY586519.1	99277	6916.3	7413.6	5662.5	6845.3	9262.5	7315.8
EU024153.1	245134	2168.5	2645.8	3242.9	3370.1	2787.4	4936.6
Y17010.1	7219	1360.1	1313.1	1962.9	2392.6	1447.3	3017.3
AY949188.1	131028	2388.7	1791.5	5012.8	6663.4	1254.8	3671.5
AB091191.1	532737	840.6	1111.9	2336.2	1022.4	546.1	900.6
GQ181142.1	578615	519.9	957.6	3035.9	790.6	681.4	960.0
AB091187.1	591807	11787.2	12527.7	13958.5	10161.8	13468.1	13804.0
EU447188.1	265915	525.5	1121.8	2963.2	715.4	672.3	684.1
AB091185.1	556961	13240.0	13415.0	20506.6	13690.0	16394.4	17998.2
EU024155.1	239548	702.7	1042.7	2152.1	1348.0	1222.4	1850.3
AB091190.1	565827	3156.0	3173.6	7217.9	3670.5	2725.8	4605.5
AB091193.1	569412	2399.2	2844.9	7829.6	4180.9	2714.0	3634.3
AB091192.1	579372	15677.8	14425.5	13004.4	14399.9	17460.1	17243.9
EU447189.1	266794	877.9	1431.7	2595.2	1087.7	828.2	1575.0
AY568512.2	111993	13180.1	7639.8	18900.3	13843.6	10586.9	14778.9
AB091181.1	584797	12158.8	10057.8	14955.8	12503.0	11446.7	12758.3
AB091189.1	570439	9865.1	10636.6	11770.1	10614.9	8576.1	11774.9
AB091184.1	584364	9887.1	10693.7	11178.2	11219.7	15253.6	15699.4
AY178065.1	103619	1417.6	2089.4	4612.4	2496.0	2162.8	2838.5
EU024170.1	244278	8581.3	6371.0	8603.0	9877.6	8455.4	6022.6
EU024175.1	256228	7738.7	6545.7	11775.4	9220.6	10323.6	7449.5
AB012916.1	34465	9806.8	8648.3	13848.7	12127.4	10117.2	9437.0
AY268163.1	91595	9048.8	7814.6	13198.6	12160.2	9534.8	7844.1
AY586517.1	98973	7619.0	7096.3	9533.5	9368.2	8326.6	7571.6
EU024176.1	239929	7208.4	6526.0	9758.5	8266.5	9212.1	6602.4
AY586515.1	107629	8350.0	7476.2	10229.6	9897.3	8877.0	7499.9
GQ337697.1	581096	5958.4	6815.4	11068.0	9457.7	8074.5	6819.5
GQ900610.1	537377	18974.8	13897.8	17223.1	16320.6	13263.4	12658.2
AB023646.1	7270	8418.4	7553.7	12540.8	11519.7	8465.7	7907.2
EU090891.1	264212	9073.5	7870.2	12963.6	12203.5	8758.1	8164.4
AY949201.1	134333	7526.2	6315.1	9918.8	8495.4	7672.0	6274.1
GQ337699.1	532689	10150.0	7667.7	9920.9	10942.2	6863.8	8975.8
EU560426.1	273601	7398.1	6739.1	10790.1	9452.6	8009.3	6643.2
EU024168.1	252056	7380.1	6802.0	8971.9	9006.0	7141.3	6990.7
EU053154.1	239216	7716.1	8298.5	12725.3	10376.8	10239.4	9097.0
AY154377.1	75813	3645.6	4586.4	7277.7	4936.7	7308.6	7894.6
AJ971354.1	138733	5509.4	3598.7	9316.8	8454.0	4949.8	5614.9
AY154368.1	75249	10714.2	9086.7	10672.0	11370.9	8198.2	9635.1
AY154378.1	76415	5124.0	3631.3	7328.6	7240.7	4811.3	5631.9
AY154367.1	77259	5003.5	5039.8	5243.5	6653.0	6305.7	6223.2
AY307365.2	137089	945.6	845.7	1324.7	1622.0	467.2	766.9

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AF448045.1 gg_id:111824 Burkholderia sp. str. SOD-6
AF448046.1 gg_id:111834 Burkholderia sp. str. SOD-7
AB495125.1 gg_id:583456 Burkholderia heleia str. SA53
AY586520.1 gg_id:103048 Burkholderia kururiensis str. LUC5
AY586516.1 gg_id:107783 Burkholderia kururiensis str. IRP416
AY586518.1 gg_id:99125 Burkholderia kururiensis str. LUC24
AY305742.1 gg_id:91555 Burkholderia mallei str. 2002734303
AF110187.1 gg_id:7240 Burkholderia mallei str. NCTC 10260
CP000010.1 gg_id:128557 Burkholderia mallei str. ATCC 23344
CP000526.1 gg_id:198878 Burkholderia mallei str. SAVP1
FJ932759.1 gg_id:537761 Burkholderia multivorans str. 103104
DQ108388.1 gg_id:159901 Burkholderia oklahomensis str. C6786 1974002358
NC_010681.1 gg_id:281436 Burkholderia phytofirmans str. PsJN
CP001053.1 gg_id:286573 Burkholderia phytofirmans str. PsJN
GQ181055.1 gg_id:553214 Burkholderia sordidicola str. BLN20
AY154369.1 gg_id:75173 Burkholderia glathei Hg 4
FJ434112.1 gg_id:368254 Burkholderia sp. str. IMER-A1-13 BCB66
AY178076.1 gg_id:99855 Burkholderia sp. CD9
GQ181054.1 gg_id:582478 Burkholderia sordidicola str. BLN14
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AY040362.1 gg_id:71813 Burkholderia terricola str. LMG 20594T
AB252074.1 gg_id:173767 Burkholderia tropica str. BF-4
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CP000614.1 gg_id:204077 Burkholderia vietnamiensis str. G4
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AF475065.1 gg_id:75398 Psychotria kirkii var. mucronata 835396 symbiont kirkii
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FJ459989.1 gg_id:567043 Burkholderia sp. L27 str. L27; IMER-A3-26
EU024181.1 gg_id:248243 Burkholderia glumae str. CIP 106418
AM502987.1 gg_id:214324 endobacteria some ectomycorrhizas ectomycorrhiza
DQ451503.1 gg_id:156722 forest soil clone FAC64
EU677404.1 gg_id:293672 Field-based stable isotope probing identities benzoic acid-metabolizing microorganis
GQ306172.1 gg_id:582115 Experimental Study Nest Microbes Borneo's Exploding Ants (Camponotus Colobopsi
AY277698.1 gg_id:101733 Psychotria nigropunctata symbiont
EU477830.1 gg_id:275692 and validation prototype -based taxonomic microarray members genus Burkholderia
DQ388536.1 gg_id:199521 Burkholderia thailandensis str. 82172
EU024180.1 gg_id:244793 Burkholderia vietnamiensis str. CIP 105875

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AF448045.1	111824	886.0	860.6	2247.8	1462.1	618.0	809.4
AF448046.1	111834	1515.3	1760.5	5049.7	3200.5	1300.2	1503.1
AB495125.1	583456	6468.0	7281.3	10313.0	8077.0	7878.1	9575.7
AY586520.1	103048	10405.5	6212.1	11275.6	12709.8	8488.1	10870.7
AY586516.1	107783	7571.1	7821.9	8208.2	8104.8	6985.2	8219.6
AY586518.1	99125	10803.9	9772.6	10000.8	10019.7	10906.0	10772.5
AY305742.1	91555	7722.5	5417.1	12837.9	9798.5	4860.5	7182.9
AF110187.1	7240	8815.4	8454.0	10474.7	14315.7	8678.3	9397.1
CP000010.1	128557	12752.8	12924.6	16598.7	14713.4	11253.6	10873.0
CP000526.1	198878	9764.4	8396.3	14932.0	11694.0	7339.9	9405.6
FJ932759.1	537761	6621.1	5723.6	12702.2	10715.5	6615.4	6310.8
DQ108388.1	159901	5163.5	5120.2	6432.7	7238.4	4796.6	4193.0
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AY154369.1	75173	4430.1	2729.4	4443.8	5866.8	3618.1	4259.0
FJ434112.1	368254	6115.9	2924.2	5482.3	7492.9	2887.3	4469.7
AY178076.1	99855	7594.0	6290.9	9766.1	11277.6	8663.9	8521.6
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AY040362.1	71813	576.2	1021.8	1894.1	898.7	605.9	820.5
AB252074.1	173767	3802.3	1659.5	2655.8	2791.7	1903.7	2443.4
AY178073.1	99382	10871.8	7512.7	16770.9	13164.3	8130.5	9102.7
CP000614.1	204077	3346.7	3194.8	8366.8	6481.3	5184.8	3923.3
U86373.1	7200	4102.8	4070.1	4708.2	3152.2	3319.2	4387.2
AF475068.1	75885	4925.0	3647.0	4719.6	6282.4	8160.4	8821.5
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AF097533.1	7253	6330.2	7127.2	8125.3	9972.4	6528.0	7242.5
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GQ306172.1	582115	2346.3	1676.0	5259.8	3611.8	1506.3	3070.7
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DQ388536.1	199521	1983.1	2684.5	4162.1	2593.5	3536.5	3193.9
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EU477825.1 gg_id:271151 and validation prototype -based taxonomic microarray members genus Burkholderia
AF093056.1 gg_id:46605 Burkholderia pseudomallei V684
AM502995.1 gg_id:214181 endobacteria some ectomycorrhizas pine root
GU123611.1 gg_id:584116 Burkholderia pseudomallei str. CEMM1336R
AM998532.2 gg_id:350434 Burkholderia cepacia str. GAH1
AAYX01000015.1 gg_id:216718 Burkholderia pseudomallei str. 305
AY949194.1 gg_id:131124 Burkholderia sp. LMG 22934 A22-1
AF364859.1 gg_id:37791 Burkholderia sp. str. AB119
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GQ306167.1 gg_id:546672 Experimental Study Nest Microbes Borneo's Exploding Ants (Camponotus Colobopsi
AB366329.1 gg_id:261292 Burkholderia sp. SBH-7
DQ103700.1 gg_id:150825 Burkholderia multivorans str. Uwc 10
AJ440715.1 gg_id:77747 Burkholderia pyrrocinia str. R1904
EF990634.2 gg_id:253304 Burkholderia cepacia str. PCL3
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EU684748.1 gg_id:355706 Burkholderia cenocepacia str. ZYB002
AB183678.1 gg_id:110590 Burkholderia plantarii str. 9411
EU477798.1 gg_id:277471 and validation prototype -based taxonomic microarray members genus Burkholderia
AB211225.1 gg_id:115316 Burkholderia cepacia str. NKCM8901
FJ434113.1 gg_id:364827 Burkholderia sp. str. IMER-A1-17 BCB57
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AY836218.1 gg_id:111169 Burkholderia phytofirmans G44-5
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GU123611.1	584116	8816.2	7281.5	14135.7	11847.9	7053.3	8079.6
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AAYX01000015.1	216718	6324.0	5054.8	10065.9	9600.2	4121.8	5355.5
AY949194.1	131124	12673.1	13515.4	8465.2	9748.5	13813.3	13351.5
AF364859.1	37791	4042.3	2726.4	10262.2	9357.3	5081.7	6022.7
NR_025097.1	558406	5552.1	5524.9	14440.5	11198.7	10125.5	9033.8
GQ306167.1	546672	957.0	1089.3	1641.0	1387.7	975.6	929.8
AB366329.1	261292	1177.4	1536.9	2109.7	1364.5	951.4	1146.9
DQ103700.1	150825	9684.2	7611.0	12811.1	11821.1	9557.3	9850.0
AJ440715.1	77747	3354.7	4471.0	11678.3	6939.0	7100.0	5523.5
EF990634.2	253304	2972.6	3119.8	2091.6	4211.0	4708.2	5708.2
AJ884849.1	174942	6642.1	7543.6	5566.8	6989.2	8067.3	6516.3
AM502989.1	205630	5800.5	2931.7	4123.0	6073.3	2321.4	4157.2
EU477810.1	271814	5258.1	5635.8	6639.8	7091.3	5664.0	5398.3
AF148556.1	74106	5463.7	5329.9	10654.2	9343.9	5429.3	6352.4
AB299597.1	243500	2206.6	2367.5	7090.2	6519.9	4098.7	5834.2
EU684748.1	355706	3454.2	3106.6	5112.7	4348.5	3053.7	4524.3
AB183678.1	110590	989.0	1804.2	5653.7	1458.8	7475.4	1656.9
EU477798.1	277471	2702.4	4490.0	6761.3	4299.3	6772.1	5342.2
AB211225.1	115316	7928.2	6612.9	6852.6	5310.9	4484.4	4919.2
FJ434113.1	364827	1219.8	1108.9	1920.9	2426.2	2583.4	3976.7
AB024310.1	7215	3122.7	3728.6	7511.1	5205.9	5754.7	5315.6
EF139178.1	185636	8736.2	3600.1	9886.6	9302.4	2788.7	5072.0
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AY836218.1	111169	9237.5	6315.4	6405.5	10836.5	6062.4	7225.0
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EU477799.1	277552	3793.8	5836.4	4347.4	3439.0	4998.9	4982.8
EU477824.1	260877	9519.5	8536.9	9617.5	11569.9	7457.6	7802.0
AB021423.1	7226	5222.6	5347.2	7657.9	7259.5	8399.1	7789.2
EF602562.1	233226	3936.2	3463.4	11228.7	7439.4	4462.8	4288.3
EU477829.1	262758	2119.1	1711.0	1427.0	2966.9	1879.9	2198.7
EF114394.1	549529	2667.9	3936.5	3758.0	4226.6	4293.4	3435.1
EF114398.1	513401	8001.6	6926.8	13078.6	11607.3	7962.9	6816.6
FJ266326.1	512661	640.0	1307.8	3142.0	1786.3	752.1	1127.6
EU024151.1	254452	9180.8	7402.8	17921.4	17179.5	8586.5	11819.5
EU477811.1	271591	5252.6	5862.9	9672.5	6875.7	7420.2	6565.2
AY741332.1	100540	9849.3	6259.1	12610.3	11726.2	6948.8	7571.4

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FM212276.1 gg_id:354442 Burkholderia cepacia str. H10 soil
AY683043.1 gg_id:151269 Burkholderia sp. str. CBMB40
GU144371.1 gg_id:579880 Burkholderia fungorum str. UFLA04-219
AB365791.1 gg_id:257466 Burkholderia sp. str. WR43
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EF178444.1 gg_id:188143 Burkholderia cepacia str. 2Pe22
EU477812.1 gg_id:258305 and validation prototype -based taxonomic microarray members genus Burkholderia
AY904767.1 gg_id:112298 Burkholderia sp. str. SEMIA 6166
CP001026.1 gg_id:263782 Burkholderia ambifaria str. MC40-6
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AY741362.1 gg_id:106783 Burkholderia cepacia str. ATCC 53130
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AB183679.1 gg_id:110091 Burkholderia plantarii str. 2396
AF042161.1 gg_id:7277 Burkholderia cepacia str. PVFi5A
AB162427.1 gg_id:102281 Burkholderia cepacia str. nao7
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AY512825.1 gg_id:106470 Burkholderia cepacia str. S74
CP001504.2 gg_id:518847 Burkholderia glumae str. BGR1
AY741343.1 gg_id:105752 Burkholderia cepacia str. ATCC 27515
EU679403.1 gg_id:280465 Burkholderia cepacia str. CAS19
EF153307.1 gg_id:187232 identification gut red imported fire ant (Solenopsis Buren) GI tract Solenopsis invicta
AF097531.1 gg_id:7251 Burkholderia multivorans str. LMG 14293
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AY221957.1 gg_id:80812 Burkholderia unamae str. SCCu-23
EU024169.1 gg_id:244233 Burkholderia pseudomallei str. BX 571966
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EU477821.1 gg_id:264315 and validation prototype -based taxonomic microarray members genus Burkholderia

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AY773194.1	108848	6427.0	2674.8	7621.7	6861.5	1873.1	3810.1
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AY741362.1	106783	9020.0	5149.2	7026.5	8613.0	6095.6	5080.0
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AF042161.1	7277	4657.2	4207.8	8608.5	7428.3	4729.8	5364.0
AB162427.1	102281	12018.7	9944.3	8998.2	8760.6	9289.8	9362.6
DQ812969.1	167754	3483.4	3586.3	8788.6	6300.8	3712.1	4809.5
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AM489502.1	224767	6166.2	5796.2	5089.3	5549.5	4006.3	5070.7
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EF153307.1	187232	1960.9	6094.9	3275.6	2745.5	2509.8	3512.0
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L28675.1	7242	7228.0	4851.0	4840.6	8482.3	9738.0	7581.9
AY268157.1	91828	9107.5	3152.8	9535.3	10349.8	1305.8	4158.7
AY221957.1	80812	6632.4	4501.9	15170.8	7351.1	7434.7	8411.1
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AY268142.1 gg_id:91013 Burkholderia cepacia str. 1998019618
EU160520.1 gg_id:317622 diagnosis central-venous infections cultivation-dependent and techniques biofilm sci
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AB299588.1 gg_id:253502 Burkholderia sp. str. 62-VN9-1W
FJ969840.1 gg_id:371448 Burkholderia cepacia str. CH9
EU447185.1 gg_id:276631 Burkholderia sp. str. SE4
AB201285.1 gg_id:112114 Burkholderia terrae str. KMY02
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AY741333.1 gg_id:100697 Burkholderia cepacia str. ATCC 17616
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EU477819.1 gg_id:275409 and validation prototype -based taxonomic microarray members genus Burkholderia
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EU047554.1 gg_id:249666 Burkholderia cepacia str. TMPSB13
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EU677398.1 gg_id:289044 Field-based stable isotope probing identities benzoic acid-metabolizing microorganis
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AF226727.1	27908	10194.3	10073.1	12653.9	11631.9	11971.9	11383.7
AY949196.1	135993	1359.0	1467.8	1346.9	2487.7	2165.0	2172.7
AY081989.1	68654	8882.2	8206.9	14328.5	11450.3	9857.8	10371.7
AY268142.1	91013	2919.3	3561.6	10545.6	7064.3	5652.0	4842.3
EU160520.1	317622	2560.1	3272.8	3266.8	2332.7	4111.7	3980.6
AB366334.1	259826	3163.5	4274.5	5127.6	6098.3	3057.2	2635.8
AB299588.1	253502	4246.3	2184.6	7608.4	6870.4	5073.2	6805.9
FJ969840.1	371448	10524.4	9104.2	8543.3	11723.5	10150.5	9370.5
EU447185.1	276631	2824.6	2538.3	2610.6	4616.0	2326.0	2192.2
AB201285.1	112114	1265.9	1899.2	3838.2	2731.6	1723.0	3596.3
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EU024177.1	240145	13959.9	16179.4	9312.5	10292.8	13313.4	12982.7
AF097530.1	7250	3037.9	3049.6	8010.7	5469.3	3362.3	4320.5
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FJ493021.1	552357	2831.5	2895.2	6259.8	4783.7	2598.2	3988.2
AY305785.1	91403	8645.5	7208.7	13152.7	10168.6	5831.6	7835.1
AY154371.1	75371	10749.4	10200.1	9597.5	13789.1	9737.5	10389.6
EF546394.1	218457	13988.2	8343.6	14508.3	16617.8	5627.8	7882.4
AY741358.1	102703	2173.6	2904.0	4083.8	3126.0	2205.6	2671.4
AY568508.2	107719	7138.3	6224.0	10842.9	9493.5	6205.4	6432.8
EU477806.1	275671	631.5	1460.4	4983.5	3463.6	1804.1	1904.0
EF139184.1	175095	3993.9	3684.1	5356.6	6427.3	2358.0	5634.7
EU477803.1	272066	5227.6	4798.5	9395.4	7230.5	5035.9	5859.9
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FJ445745.1	542551	8147.9	6414.7	11526.8	9887.7	8421.5	6476.0
EU447182.1	270872	5530.4	5447.7	15156.4	10101.9	6389.1	6114.8
AJ938144.1	139689	2219.7	3448.1	6441.4	4140.7	4695.3	4116.1
EU047554.1	249666	5977.3	3927.4	7931.3	8716.0	5018.7	4800.2
EU246850.1	245565	2886.3	3064.0	7518.5	4952.7	3168.0	4262.5
AF093058.1	39013	4986.2	3489.3	7524.2	6118.6	2877.0	4217.4
U91570.1	7210	1890.0	1459.9	3076.1	2688.9	1135.6	1694.8
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AF164043.2 gg_id:69874 diazotroph str. AB48
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NR_029212.1 gg_id:541985 Burkholderia phenazinium str. 1; LMG 2247
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AJ616912.2	99823	8087.0	5578.7	8970.1	8664.8	6663.2	5598.1
AY677088.1	138801	3644.5	3688.1	10486.2	8033.5	4056.4	4746.6
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DQ514537.1	161156	4809.2	5250.7	4946.3	6076.4	4391.4	6141.6
AB162428.1	102436	14410.2	12247.3	11998.6	10499.9	9589.9	10664.8
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U96927.1	7279	16782.9	15750.3	6181.7	13241.3	11304.1	10688.8
FJ266321.1	560446	480.3	874.2	1401.4	1771.8	408.3	727.4
AY040365.1	71936	3600.9	3398.7	6799.8	7528.3	3266.2	4607.4
CP000440.1	163210	4153.9	3821.7	11594.7	7511.6	4597.0	4295.3
AJ884850.1	188950	7928.9	7959.8	13704.2	8884.2	8840.2	7728.4
EU477822.1	272204	1408.2	2353.7	3940.0	2660.2	1695.5	2027.8
CP000440.1	163213	4618.5	5430.9	12588.8	9620.3	7940.4	6781.5
EU477809.1	276295	3516.0	4684.5	7746.5	6084.2	4744.2	5007.9
EU477814.1	262558	6060.3	4641.9	9561.6	6725.5	3189.9	4081.2
AB030584.1	31991	4846.5	4594.5	8794.9	6512.7	4932.9	5728.7
AF074712.1	7214	3120.2	1979.8	6660.5	5598.7	2609.8	4245.2
AB191210.1	114735	5234.0	6546.5	6244.3	8748.7	11740.3	11175.2
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AF148555.1	72468	2920.4	3659.2	10241.5	7359.2	5537.6	4623.4
AF043302.1	7249	4357.3	3807.2	8787.9	7529.9	4216.8	5048.7
U96932.1	7246	8447.2	7801.7	10189.8	8849.6	9832.3	7840.4
AY178057.1	107786	2892.6	1295.3	1543.6	5087.2	594.4	1485.9
FJ434117.1	362426	8563.9	8183.7	11554.8	10985.2	11401.4	12377.0
AY486372.1	99847	9641.6	8593.9	12769.4	11091.4	9972.8	9306.9

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AJ440714.1 gg_id:78142 Burkholderia pyrrocinia str. R13058
AB088048.1 gg_id:77828 Burkholderia sp. str. VE22

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AY391283.1	96893	3563.4	1768.9	13116.3	4801.6	1482.3	2034.3
FJ466367.1	547752	8095.0	5216.9	8627.4	9256.3	4376.7	6126.9
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DQ156084.1	139190	3397.5	4269.1	4305.5	5833.6	3764.8	6119.7
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EU477823.1	273722	1473.0	2868.8	3538.8	2281.5	2623.2	2797.9
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AB110089.1	87062	5351.3	5416.9	15063.6	9897.4	7371.3	6423.9
AY677089.1	139095	3824.2	3419.9	7992.9	6621.2	3861.2	4809.6
U91838.1	7237	5666.6	6037.1	6306.8	8233.5	5132.0	6162.2
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AM502993.1 gg_id:205234 endobacteria some ectomycorrhizas ectomycorrhiza
EU024147.1 gg_id:245512 Burkholderia sp. str. CIP 105081
AY949198.1 gg_id:132721 Burkholderia sp. LMG 21262 A13-5
AM284970.1 gg_id:159660 Burkholderia nodosa R-22632
AB232335.1 gg_id:153688 Burkholderia sp. str. SFA3
AJ551104.1 gg_id:94022 Burkholderia sp. wp26
AB091761.1 gg_id:59707 Burkholderia cepacia
NZ_ABBP01001245.1 gg_id:259644 Burkholderia pseudomallei str. 112
AB114607.1 gg_id:107108 Burkholderia cepacia str. CNR22
AY792254.1 gg_id:119349 Humic Lake clone CrystalBog572G9
AB288301.1 gg_id:211076 Burkholderia sp. str. BCB-57
EU497966.1 gg_id:269721 Burkholderia cepacia str. 1-3b
DQ855426.1 gg_id:166835 Burkholderia hospita str. MM1710
EU024157.1 gg_id:249316 Burkholderia caledonica str. CIP 107098
AY268156.1 gg_id:91320 Burkholderia cepacia str. 1998003405
EF373556.1 gg_id:215882 Burkholderia cepacia str. AW201
AF074711.1 gg_id:7213 Burkholderia sp. EN-B3
AF408946.1 gg_id:102140 Burkholderia sp. str. Ellin104
GU123610.1 gg_id:574252 Burkholderia pseudomallei str. CEMMBP5
EF113108.1 gg_id:194598 Burkholderia cepacia
EU563934.1 gg_id:258183 Burkholderia vietnamiensis str. WPB
AY741353.1 gg_id:101935 Burkholderia cepacia str. ATCC 53642
GQ169807.1 gg_id:583719 Burkholderia cepacia str. B1700
EU477808.1 gg_id:261284 and validation prototype -based taxonomic microarray members genus Burkholderia
AY268141.1 gg_id:91654 Burkholderia cepacia str. 1996034502
GQ181027.1 gg_id:581174 Burkholderia phytofirmans str. LNW6
FJ434114.1 gg_id:360691 Burkholderia sp. str. IMER-A1-16 BCB20
EU399922.1 gg_id:266408 Burkholderia sp. str. CAF324
AB537485.1 gg_id:586257 Burkholderia acidipaludis str. NBRC 101816
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AY677087.1 gg_id:139053 Burkholderia cepacia str. LMG 12614t2 TC62
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FJ842655.1 gg_id:568984 Burkholderia sp. str. DBTB
AJ131790.1 gg_id:7238 Burkholderia pseudomallei
EU477837.1 gg_id:265147 and validation prototype -based taxonomic microarray members genus Burkholderia
AJ251633.1 gg_id:38919 Gigaspora margarita strain WV205A-5 symbiont gigasporarum

FJ025134.1	308186	798.8	1094.4	1980.8	1625.2	1274.0	1607.7
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EU024147.1	245512	8133.5	9645.1	3827.3	7662.0	7167.5	7953.2
AY949198.1	132721	2498.9	2048.3	4176.3	5226.6	2809.2	3874.6
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AB232335.1	153688	2852.9	2379.3	3823.8	4499.0	1889.1	1777.4
AJ551104.1	94022	3723.1	3813.8	6442.3	5230.7	2593.9	3746.1
AB091761.1	59707	3483.6	3731.2	9710.7	6827.7	3769.3	4821.2
NZ_ABBP01001245.1	259644	7609.4	7709.2	10207.5	9037.7	8101.7	8939.6
AB114607.1	107108	9600.5	8155.5	15087.9	12919.3	9641.7	8753.9
AY792254.1	119349	9157.0	9239.5	8774.9	10272.7	7967.8	8390.7
AB288301.1	211076	9160.2	3228.5	8500.7	11126.6	3724.5	6662.2
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DQ855426.1	166835	8550.9	9082.2	9393.3	9398.4	12380.4	10229.2
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AY268156.1	91320	6199.7	5982.6	16494.1	11456.7	6881.3	6312.2
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AY741353.1	101935	6477.0	6507.0	15140.7	11372.0	6848.3	7067.0
GQ169807.1	583719	8249.4	6738.3	10015.6	10105.3	5977.2	8646.4
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AY268141.1	91654	3179.2	3978.9	11798.2	7977.4	5907.0	5113.3
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DQ387434.1	224812	2961.4	1592.7	3390.5	5647.2	920.6	1974.1
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s__Cupriavidus gilardii	14404
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AJ251636.1 gg_id:28964 Scutellospora castanea strain BEG1 symbiont gigasporarum
AJ251635.1 gg_id:50390 Scutellospora persica strain E09 symbiont
FJ479009.1 gg_id:512517 species richness estimates obtained nearly and simulated pyrosequencing-generated
AF476077.1 gg_id:63963 Australicoccus grevilleae symbiont
AF476084.1 gg_id:63959 Erium globosum symbiont
AF476090.1 gg_id:63954 Nipaecoccus exocarpi symbiont
AF476081.1 gg_id:63962 Cyphonococcus alpinus symbiont
AF476079.1 gg_id:63964 Antonina pretiosa symbiont
AF476092.1 gg_id:63949 Planococcus ficus symbiont
GQ284441.1 gg_id:593696 Chitinimonas taiwanensis str. TSWCSN23
GQ284440.1 gg_id:548727 Chitinimonas taiwanensis str. TSWCSN26
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DQ256728.1 gg_id:144420 Chitinimonas koreensis str. R2A43-10
AY323827.2 gg_id:107650 Chitinimonas taiwanensis str. cf
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AY040355.1 gg_id:72788 Wautersia campinensis str. LMG 20576
EF114425.1 gg_id:509683 Cupriavidus gilardii MSMB8
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EU915714.1 gg_id:336731 Cupriavidus taiwanensis str. G
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GQ255543.1 gg_id:580571 Cupriavidus sp. str. MBT14
AB208547.1 gg_id:140391 Cupriavidus necator str. NH9
GU167922.1 gg_id:582706 Cupriavidus sp. str. 2CSb-7
AB015605.1 gg_id:7389 Wautersia eutropha str. KT1
EU024156.1 gg_id:241006 Cupriavidus oxalaticus str. CIP 107389
AB232327.1 gg_id:150729 Ralstonia sp. str. IFA3
EU024161.1 gg_id:239364 Cupriavidus metallidurans str. CIP 107179
EU024165.1 gg_id:239356 Cupriavidus pauculus str. CIP 105943
AB109753.1 gg_id:85415 Wautersia paucula str. KF709
EU827495.1 gg_id:310258 Ralstonia eutropha str. JMP134
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AJ251635.1	50390	914.5	1414.7	2977.4	1735.2	1306.5	1556.6
FJ479009.1	512517	6760.0	6394.0	9024.5	8093.7	11584.2	8910.6
AF476077.1	63963	13714.7	19087.5	11512.2	11348.8	14816.2	15243.1
AF476084.1	63959	62.5	193.4	37.4	294.9	641.3	317.4
AF476090.1	63954	9497.9	8420.0	8200.7	8056.3	9254.7	8802.6
AF476081.1	63962	1322.1	2506.3	2398.4	1467.4	2534.0	3311.8
AF476079.1	63964	4981.1	5481.2	3514.7	4354.4	7628.1	8729.7
AF476092.1	63949	65.9	104.0	284.3	101.6	97.9	88.5
GQ284441.1	593696	3939.3	3247.9	7429.7	7085.2	4851.3	5057.7
GQ284440.1	548727	4970.0	4153.2	6693.9	6566.1	4598.5	4911.7
GQ284446.1	541884	4295.5	3393.3	6588.3	6505.6	4892.3	4825.8
DQ256728.1	144420	3640.1	3528.4	3317.7	3071.5	1957.1	1901.0
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AY047217.1	50666	1789.3	1460.3	3207.4	6053.9	2538.4	3649.7
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EU024159.1	243432	3640.7	2602.9	8440.9	7948.0	5648.8	6224.4
EU169175.1	243952	921.3	1076.3	2553.4	1311.9	3797.7	5018.0
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AY860228.1	111886	1238.4	1428.5	3160.5	3139.4	1730.4	3679.2
AY860231.1	111474	991.8	1368.3	4604.4	2838.6	3626.2	5749.9
AY860230.1	111539	207.9	326.6	587.2	277.1	448.8	562.6
EU915714.1	336731	1870.2	1640.6	4717.7	3430.6	3391.7	5995.3
AY860226.1	112181	916.7	1063.1	2160.3	2118.9	1492.9	2945.4
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EU024163.1	251612	1521.8	1648.2	2203.4	3904.1	3783.4	7080.1
GQ255543.1	580571	3050.5	4162.3	8973.2	4669.6	6166.5	10103.1
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GU167922.1	582706	12986.4	10645.5	7630.0	9018.3	9426.1	8374.0
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EU024156.1	241006	11768.3	9516.4	3292.4	6533.7	8667.2	7406.2
AB232327.1	150729	3316.7	2481.1	3692.9	4706.1	6302.4	10791.1
EU024161.1	239364	2714.0	2226.9	3116.1	6375.3	4841.6	6550.7
EU024165.1	239356	3003.8	2319.7	3309.9	6295.1	4938.0	5791.9
AB109753.1	85415	54.3	139.4	169.6	103.7	3466.1	990.5
EU827495.1	310258	3660.4	3436.4	3969.5	4615.9	3737.1	7087.3
GU202015.1	576596	2814.8	2709.7	1652.7	3975.6	4028.6	5748.2
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EF446928.1 gg_id:214206 Cupriavidus taiwanensis str. AAJ14
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GQ342296.1 gg_id:538911 Cupriavidus necator str. CG-T3
AF067833.1 gg_id:7397 Ralstonia sp. str. TFD41
AY583652.1 gg_id:102442 Ralstonia sp. str. 1-1
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AY571787.1 gg_id:100095 Ralstonia sp. str. 1-1
AY860242.1 gg_id:111723 Cupriavidus respiraculi str. AU4630
EU447184.1 gg_id:261584 Cupriavidus basilensis str. SE15
D87999.1 gg_id:7386 Cupriavidus necator str. DSM 2839
AB007995.1 gg_id:58406 Wautersia eutropha str. P11
EF114429.1 gg_id:545936 Cupriavidus gilardii MSMB32
AF251026.1 gg_id:41961 Ralstonia sp. str. LD35
AY860237.1 gg_id:111546 Cupriavidus respiraculi str. AU3775
D88001.1 gg_id:7387 Ralstonia sp. str. CT14
AF312022.1 gg_id:73500 Wautersia basilensis str. DSM 11853
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AY860227.1 gg_id:111839 Cupriavidus gilardii str. AU3713
AY860234.1 gg_id:111890 Cupriavidus metallidurans str. AU4057
AY860250.1 gg_id:111665 Ralstonia sp. str. AU5980
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AB109778.1 gg_id:83846 Wautersia basilensis str. KF708
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AF361022.1 gg_id:33253 Ralstonia sp. str. NAH8
AB104447.1 gg_id:111989 Wautersia numadzuensis str. TE26
AB271141.1 gg_id:168999 Cupriavidus gilardii str. MXC3-9
EU827493.1 gg_id:325237 Cupriavidus respiraculi str. TFD48
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AF500587.1 gg_id:56268 Wautersia respiraculi str. AU3369
DQ298326.1 gg_id:152771 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
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Y10825.1 gg_id:7382 Wautersia eutropha str. DS185
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AY860242.1	111723	11297.2	9289.2	10879.9	13777.8	16921.4	13684.6
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D87999.1	7386	5074.8	3588.5	6026.3	10701.5	8152.6	10769.1
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EF114429.1	545936	3366.7	3456.2	2994.6	6413.7	5172.2	8673.8
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AY860237.1	111546	4432.5	2716.4	10085.4	4843.4	3138.9	4287.7
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DQ409082.1	154472	2532.9	2383.8	4114.7	6617.3	3192.3	3822.1
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AY303977.1	88067	6128.4	5126.4	5178.7	5671.8	6094.4	9028.7
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AB104447.1	111989	21243.6	21759.5	23990.4	19398.3	22954.8	20260.0
AB271141.1	168999	13315.4	13291.8	9417.4	11354.8	14070.8	12382.8
EU827493.1	325237	5278.1	3578.7	3831.6	4459.0	5100.2	5488.1
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AF500587.1	56268	10007.8	9899.9	14053.7	9366.7	7302.7	7966.8
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AY568502.2	106836	5966.1	4854.1	3360.4	7073.2	8107.0	6385.6
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AB167180.1	107898	5232.6	3920.3	7513.8	9920.7	6422.9	8482.5
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AM905275.1	327185	3743.5	2845.8	3548.5	4474.6	9037.9	9432.5
AF312021.1	70450	1998.1	2254.9	8261.4	6257.2	6703.9	9203.2
AY860235.1	112054	2767.8	2395.9	3648.3	5839.1	5139.6	7268.5
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GQ074337.1 gg_id:389328 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161g
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AY268172.1 gg_id:89390 Pandoraea apista str. CCUG 38412
Y09879.1 gg_id:7183 Pandoraea norimbergensis
AY268174.1 gg_id:88183 Pandoraea norimbergensis str. CCUG 39188
EF596910.1 gg_id:230684 Pandoraea pnomenusa str. B-356
AY268168.1 gg_id:88090 Pandoraea pnomenusa str. 2001008157
AB244466.1 gg_id:240824 Pandoraea pulmonicola str. C10-2
DQ837222.1 gg_id:255307 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_3
AY677092.1 gg_id:139269 Pandoraea sputorum TC84
AM921627.1 gg_id:238898 Pandoraea sputorum PhyCEm-128
AB118229.1 gg_id:105307 Pandoraea sp. PAMU-2.78
AY693821.1 gg_id:107349 anaerobic sludge clone EUB64
AF139176.1 gg_id:72789 Pandoraea sputorum str. LMG 18819
AM110110.2 gg_id:139991 Polynucleobacter sp. str. MWH-Braz-FAM3C
AF534432.1 gg_id:85148 Toolik Lake main station at 3 m depth clone TLM08/TLMdgge25a proteobacterium
AF534427.1 gg_id:86341 Toolik Lake main station at 3 m depth clone TLM03/TLMdgge33 proteobacterium
EF667903.1 gg_id:240040 Long-term maintenance species-specific microbiota basal metazoan Hydra epitheliun
FM208180.1 gg_id:320042 Polynucleobacter sp. MWH-PoolGreenA3
AY947963.1 gg_id:142102 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
EU800885.1 gg_id:352838 It's all ranking aquatic Delaware Bay NJ clone 2C229123
EU803597.1 gg_id:315886 It's all ranking aquatic Lake Gatun clone 5C231196
AJ811013.1 gg_id:106508 Polynucleobacter sp. FC1
AJ270258.1 gg_id:48140 Ralstonia mannitolilytica str. LMG6866
EU024152.1 gg_id:251899 Ralstonia mannitolilytica str. CIP 107281
DQ924950.1 gg_id:249852 Ralstonia solanacearum str. SL341
AB024604.1 gg_id:50898 Ralstonia solanacearum MAFF 211266
AY464966.1 gg_id:114414 Ralstonia syzygii str. T327
FJ193945.1 gg_id:320934 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
DQ997838.1 gg_id:177991 Ralstonia pickettii str. HM-1
EF562212.1 gg_id:247420 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
AB024608.1 gg_id:40253 Ralstonia solanacearum MAFF 301559
FJ193860.1 gg_id:338003 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ194034.1 gg_id:308094 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EF562231.1 gg_id:249054 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
FJ191398.1 gg_id:326241 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EF207564.1 gg_id:210668 mangrove system sediment
FJ193764.1 gg_id:350437 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
AJ583178.1 gg_id:95147 radioactive site ground water clone S15D-MN15
FJ193746.1 gg_id:349604 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi

GQ001271.1	508389	7815.2	6067.0	9614.6	9046.6	5502.3	9074.6
GQ074337.1	389328	4295.1	4053.7	6224.8	6383.6	5042.4	7771.1
AB366174.1	239543	1810.4	2065.0	4665.9	3183.9	3146.7	2194.7
AY268172.1	89390	3566.5	5355.6	8464.0	5947.5	7461.9	6972.8
Y09879.1	7183	6549.0	8011.7	12307.7	9660.4	13648.9	10983.1
AY268174.1	88183	9678.0	10471.4	17940.5	10751.1	13204.9	12319.0
EF596910.1	230684	9048.8	7953.9	11532.7	8981.8	8889.0	8704.8
AY268168.1	88090	3642.1	3752.9	7340.9	5234.1	3769.8	4025.4
AB244466.1	240824	10539.1	9851.1	11637.0	8522.5	8506.5	9025.4
DQ837222.1	255307	15857.5	15854.9	14229.0	17249.4	11139.4	13370.7
AY677092.1	139269	2214.8	3613.4	9332.4	2477.0	2813.5	1931.9
AM921627.1	238898	12095.2	9456.6	16307.3	12282.5	7849.5	9502.1
AB118229.1	105307	5556.8	6559.6	12061.0	6841.0	6276.9	5661.2
AY693821.1	107349	15126.5	16526.0	18795.1	12874.2	18918.3	16669.8
AF139176.1	72789	3726.6	4982.0	5271.9	4942.7	4307.7	5958.9
AM110110.2	139991	4135.7	1592.4	4582.5	8737.9	2350.9	5707.7
AF534432.1	85148	1224.8	1370.0	3545.9	4307.0	1956.6	1387.6
AF534427.1	86341	10278.2	9122.6	10362.3	17337.3	7442.4	10398.3
EF667903.1	240040	6033.3	4743.1	11605.2	16711.6	4295.6	4359.0
FM208180.1	320042	5908.9	4484.6	16157.3	19200.4	3414.4	5097.0
AY947963.1	142102	9532.4	11415.3	11839.9	15035.5	2063.6	3626.1
EU800885.1	352838	7291.1	7331.5	13082.8	12769.4	10980.6	6941.2
EU803597.1	315886	5935.6	4402.8	4764.2	8347.7	3924.0	3682.5
AJ811013.1	106508	7525.9	7272.1	18695.1	19658.4	7078.7	7652.4
AJ270258.1	48140	3475.0	3357.1	4920.8	6986.8	9593.9	15347.9
EU024152.1	251899	1954.1	2138.9	4649.0	5277.3	10740.0	16563.5
DQ924950.1	249852	4449.0	4228.9	6358.4	11015.5	10445.3	15205.8
AB024604.1	50898	1895.5	1939.1	2413.6	4934.5	5698.3	11012.4
AY464966.1	114414	11869.3	11779.9	9739.5	10451.1	14946.4	18614.2
FJ193945.1	320934	12457.9	11682.7	12165.0	12424.0	19157.7	21491.5
DQ997838.1	177991	13547.4	12760.7	11656.1	14071.8	18111.4	19868.4
EF562212.1	247420	6848.2	5499.4	6527.7	10193.9	9803.5	15875.2
AB024608.1	40253	5937.3	5742.9	10287.6	10328.2	11719.2	18765.6
FJ193860.1	338003	1155.7	1432.0	3421.9	5892.3	8891.9	15187.9
FJ194034.1	308094	10297.1	11072.2	7449.4	7696.8	16170.4	19738.9
EF562231.1	249054	13918.6	11495.5	12025.8	17417.6	18666.6	21913.7
FJ191398.1	326241	1296.7	1424.7	1900.2	2729.7	10738.3	19327.5
EF207564.1	210668	2690.2	2584.3	5656.2	7501.0	9525.6	15936.8
FJ193764.1	350437	15344.4	12433.9	10255.9	13946.7	17190.9	22458.3
AJ583178.1	95147	9474.3	8054.0	8769.5	10590.2	12721.0	16036.2
FJ193746.1	349604	10811.5	10384.6	11419.8	13970.6	15514.7	19625.1

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AY464953.1 gg_id:113678 Ralstonia solanacearum str. 28MF
AY043378.1 gg_id:112275 Ralstonia mannitolilytica str. AU428
FJ191418.1 gg_id:310934 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EF688395.1 gg_id:252030 soil clone F6-168
EF562200.1 gg_id:246230 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
FJ193846.1 gg_id:352582 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ193974.1 gg_id:332274 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ192332.1 gg_id:324427 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
NW_002196521.1 gg_id:341686 Ralstonia solanacearum str. MolK2
FJ821603.1 gg_id:563550 Ralstonia sp. str. TPS8
FJ191397.1 gg_id:309765 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ193962.1 gg_id:323373 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ193740.1 gg_id:308235 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EF554882.1 gg_id:223957 Ralstonia sp. str. EF38
AY646884.1 gg_id:103925 Ralstonia mannitolilytica A55
FJ193891.1 gg_id:341457 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EF016361.1 gg_id:184466 Ralstonia solanacearum str. LMG 2299
FJ192336.1 gg_id:305713 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ193886.1 gg_id:311507 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EF600590.1 gg_id:299883 leaf litter clone E2-41
AB021403.1 gg_id:7408 Ralstonia syzygii str. ATCC 49543T
DQ256353.1 gg_id:143763 subsurface water clone EV818BHEB5102702SAS31
EU234261.1 gg_id:236043 river and un techniques downstream Wang Yang River receiving penicillin G producti
FJ625332.1 gg_id:511989 Influence lead contamination on boreal pine forest soil clone HF_M_29
CU466909.1 gg_id:313184 Evry wastewater treatment plant anoxic basin clone
AB089482.1 gg_id:96705 Derxia gummosa str. IAM 13946
EU304284.1 gg_id:244827 Ralstonia sp. str. 22
FJ516875.1 gg_id:558389 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s
CU927753.1 gg_id:558915 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ484886.1 gg_id:512042 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
EU133821.1 gg_id:253342 tallgrass prarie soil clone FFCH11971
EU799756.1 gg_id:319986 It's all ranking aquatic Newport Harbour RI clone 1C227401
FJ167462.1 gg_id:310487 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
DQ450176.1 gg_id:151384 (Uruguay) Atlantic coastal lagoon clone R7C70
AJ853520.1 gg_id:110392 landfill leachate clone GZKB25
EU491796.1 gg_id:260119 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ612332.1 gg_id:545233 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.1.39
EF654710.1 gg_id:236325 suspended sludge anammox reactor clone KIST-JJY041
AB487015.1 gg_id:546434 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
AY218566.1 gg_id:81664 penguin droppings sediments clone KD1-79
EU703319.1 gg_id:412714 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH193

AY464953.1	113678	6109.8	5817.7	10210.1	10810.8	10918.3	17711.9
AY043378.1	112275	1545.9	1788.1	3786.7	4923.1	8687.2	15013.4
FJ191418.1	310934	3338.9	4126.1	5455.1	6744.3	14794.0	16092.4
EF688395.1	252030	13861.1	12139.1	8481.4	14533.2	11480.0	14311.1
EF562200.1	246230	12575.8	13148.9	12535.3	14302.4	17612.2	18468.1
FJ193846.1	352582	7423.3	9055.8	10725.5	13926.3	13478.4	18841.7
FJ193974.1	332274	4316.4	4724.3	4127.1	4446.5	10761.7	17752.4
FJ192332.1	324427	9821.2	6919.6	8568.1	13324.4	13481.9	18783.8
NW_002196521.1	341686	4632.7	3843.0	5235.2	9103.9	8312.9	11905.7
FJ821603.1	563550	6346.4	5990.5	10318.3	12284.8	13314.7	15051.2
FJ191397.1	309765	2299.3	2453.4	2991.6	3791.0	11376.5	19653.1
FJ193962.1	323373	15769.2	14946.6	10831.5	14469.2	18933.7	21680.2
FJ193740.1	308235	13669.6	11473.9	5428.4	13501.3	17245.5	19730.3
EF554882.1	223957	8893.7	6933.2	6181.2	13200.3	17776.9	20042.9
AY646884.1	103925	1567.6	2054.2	3755.3	5342.5	9493.6	15667.1
FJ193891.1	341457	11665.2	8879.6	5942.9	11328.6	12290.2	16705.4
EF016361.1	184466	7133.2	6401.4	7809.7	12362.8	10366.2	16115.4
FJ192336.1	305713	15096.5	12728.5	10471.2	16632.8	18413.1	19743.8
FJ193886.1	311507	7050.7	5728.8	7348.5	8940.1	13942.8	19419.3
EF600590.1	299883	11580.6	9495.3	14145.0	14881.5	14198.1	17881.5
AB021403.1	7408	12822.6	11977.1	10811.2	14869.4	15524.1	19833.1
DQ256353.1	143763	4648.8	5126.1	5149.0	6433.1	1119.4	2697.5
EU234261.1	236043	10101.3	11749.0	14393.3	10033.9	6295.9	8150.8
FJ625332.1	511989	4623.3	4457.8	4601.8	6560.0	1431.0	3072.0
CU466909.1	313184	755.1	1318.2	4116.4	956.5	1050.0	1289.2
AB089482.1	96705	362.3	440.2	386.7	237.0	284.6	403.5
EU304284.1	244827	1696.0	1597.0	4523.0	6375.9	4109.4	6162.5
FJ516875.1	558389	5712.3	4367.6	6561.6	9677.9	3680.2	4649.3
CU927753.1	558915	4227.2	5865.7	6300.8	6860.8	6307.8	6967.4
FJ484886.1	512042	3583.9	4714.7	2311.4	3503.5	3286.1	3223.0
EU133821.1	253342	8022.3	8434.5	7687.6	6906.8	10137.7	7711.4
EU799756.1	319986	237.8	316.9	615.6	2676.5	245.5	615.1
FJ167462.1	310487	6163.1	6467.6	7877.3	6995.3	9523.8	11885.9
DQ450176.1	151384	4009.0	4770.8	4483.2	4676.3	6916.6	6633.9
AJ853520.1	110392	3030.7	4105.5	3746.4	5199.3	2678.7	3579.9
EU491796.1	260119	4472.0	5219.5	5324.3	5833.0	5185.1	8200.3
FJ612332.1	545233	1839.1	4004.2	4354.7	5905.4	3180.8	5121.0
EF654710.1	236325	770.3	1369.1	1193.1	1453.6	1085.9	1780.3
AB487015.1	546434	3687.6	4486.2	3388.3	4831.0	4413.8	3667.3
AY218566.1	81664	5958.9	5140.6	6204.4	7974.7	4747.1	7596.7
EU703319.1	412714	4139.6	3649.4	4980.4	5675.8	781.0	2201.3

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CU466912.1 gg_id:355680 Evry wastewater treatment plant anoxic basin clone
AY921755.1 gg_id:113342 farm soil clone AKYH739
EU802154.1 gg_id:324381 It's all ranking aquatic Chesapeake Bay MD clone 3C003572
EF397578.1 gg_id:287984 Burkholderia sp. str. ATSB16
AB240293.1 gg_id:141532 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
FJ375442.1 gg_id:558588 T-RFLP powerful tool rapid assessment cells microbial fuel cell sheet carbon cloth ano
FJ612382.1 gg_id:567560 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.3.32
AY922020.1 gg_id:113843 farm soil clone AKYG464
FJ167492.1 gg_id:325718 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
AY570587.1 gg_id:108463 biodegraded Canadian oil reservoir clone PL-33B5
GQ010467.1 gg_id:499198 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ230924.1 gg_id:326020 under Level Antibiotic Selection Pressures river water clone F2
AY509453.2 gg_id:103790 freshwater clone LiUU-5-131
FJ674610.1 gg_id:515098 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF516760.1 gg_id:225714 grassland soil clone FCPS725
AB252925.1 gg_id:170130 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 57
EU727457.1 gg_id:354510 Ralstonia sp. str. JOS55-1
GQ500805.1 gg_id:570888 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
GQ389057.1 gg_id:591556 quality deterioration drinking system during serious red water outbreak clone S13
AM850114.1 gg_id:249856 Acidovorax avenae subsp. citrulli Med-H
AM084006.1 gg_id:140023 Acidovorax sp. str. R-24608
EU434539.1 gg_id:264675 Acidovorax defluvii str. b322
EU434519.1 gg_id:275328 Acidovorax defluvii str. b224
EU434529.1 gg_id:272063 Acidovorax defluvii str. b336
EU434535.1 gg_id:276678 Acidovorax defluvii str. b256
GQ284432.1 gg_id:533201 Acidovorax delafieldii str. PCWCS38
GQ284426.1 gg_id:555950 Acidovorax delafieldii str. THWCSN42
GQ284428.1 gg_id:592118 Acidovorax facilis str. THWCSN37
GQ284431.1 gg_id:589089 Acidovorax delafieldii str. THWCSN5
GQ284423.1 gg_id:552122 Acidovorax delafieldii str. THWCSN54
NR_028714.1 gg_id:574463 Acidovorax delafieldii str. 133; ATCC 17505
GQ284434.1 gg_id:593931 Acidovorax delafieldii str. PCWCS28
EU730927.1 gg_id:315092 Acidovorax facilis str. 228
EU304287.1 gg_id:251328 Acidovorax sp. str. 75
Y18616.1 gg_id:7043 Acidovorax defluvii str. BSB411
AB487337.1 gg_id:553499 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EU104261.1 gg_id:346700 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ105731.1 gg_id:374744 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GU372409.1 gg_id:575562 Acidovorax sp. str. S7
GQ106011.1 gg_id:431652 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw

EU800673.1	333534	2522.9	5211.2	6063.9	7425.1	3558.3	4611.9
CU466912.1	355680	3588.5	3636.2	3633.1	7378.2	5350.8	10296.9
AY921755.1	113342	9894.8	10950.6	4698.6	8023.5	8327.0	9208.1
EU802154.1	324381	9172.2	4528.5	13796.0	12832.9	2827.3	3305.0
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AB240293.1	141532	1926.5	735.5	1153.6	2945.8	434.2	1133.2
FJ375442.1	558588	761.4	1358.2	1826.0	1280.4	417.7	622.1
FJ612382.1	567560	10846.9	11303.8	13945.4	12564.4	12852.5	9765.7
AY922020.1	113843	1190.7	2443.9	2614.6	2051.7	575.3	2217.6
FJ167492.1	325718	4309.8	3986.9	4891.4	5949.7	4232.1	6496.6
AY570587.1	108463	11820.3	10048.2	12021.0	9333.4	8744.0	9169.8
GQ010467.1	499198	10216.0	10937.1	6569.6	10177.5	8447.4	11616.6
FJ230924.1	326020	10201.7	6950.4	10124.7	10351.8	2944.5	3796.3
AY509453.2	103790	2341.5	1665.2	4707.4	3421.6	2862.1	2198.6
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AB252925.1	170130	2138.2	2363.3	4823.3	2570.3	2013.2	1906.3
EU727457.1	354510	4698.8	4560.1	3589.3	4276.5	7558.4	11541.9
GQ500805.1	570888	3198.5	3652.1	6411.8	5269.3	1208.4	2794.1
GQ389057.1	591556	7530.9	5988.2	8986.4	10101.1	8241.6	6567.0
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AM084006.1	140023	13833.6	7151.3	13356.2	15609.7	4957.3	8118.1
EU434539.1	264675	6966.2	5361.2	10308.0	10018.1	4240.3	8006.1
EU434519.1	275328	8013.6	4933.1	8142.1	10845.9	4559.6	7697.1
EU434529.1	272063	10090.8	4758.3	12205.1	12950.5	4219.0	7701.0
EU434535.1	276678	19757.8	19430.4	22090.3	17021.7	19431.6	17234.6
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GQ284426.1	555950	2922.5	1867.9	3568.8	4037.6	1118.6	3729.0
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EU730927.1	315092	8020.6	3499.3	9443.6	8073.5	2161.4	5183.1
EU304287.1	251328	8278.1	6132.9	4677.0	9318.6	7993.5	8033.0
Y18616.1	7043	11025.4	5942.4	17199.0	15127.9	5014.5	9815.2
AB487337.1	553499	1219.4	1436.0	6185.9	3029.9	1331.1	4134.3
EU104261.1	346700	10060.9	7194.9	9741.2	10483.7	5529.6	7863.0
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CU466871.1 gg_id:339277 Evry wastewater treatment plant anoxic basin clone
FJ593725.1 gg_id:531432 midgut tropical caterpillars fed on diets larvae clone CLSM148
AY093698.1 gg_id:55345 Acidovorax sp. str. 'smarlab 133815'
GQ091955.1 gg_id:414179 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB269774.1 gg_id:208383 Acidovorax delafieldii str. HYY0511-SK09
GQ107139.1 gg_id:397297 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
EU202950.1 gg_id:251020 Linking -situ microbial identity and functionality without bias groundwater naphthale
GQ102018.1 gg_id:387956 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502e06c1
DQ264575.1 gg_id:143236 universal microarray broader than typical library when sampling subsurface groundv
AJ400840.1 gg_id:74685 Acidovorax wohlfahrtii str. B2/74
AB008429.1 gg_id:7063 Comamonas sp. str. MBIC3885 E6
AB167175.1 gg_id:107894 Acidovorax sp. str. c303
GQ107342.1 gg_id:440564 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
AF078762.1 gg_id:7047 Acidovorax avenae subsp. cattleyae str. NCPPB 961 subsp.
GQ068971.1 gg_id:447274 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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FJ560467.1 gg_id:546272 Acidovorax sp. str. SD2
AM084008.1 gg_id:140621 Acidovorax sp. str. R-24614
GQ022385.1 gg_id:487284 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
FM213427.1 gg_id:327583 Chemosynthetic Bivalvia species mud volcanoes Gulf Cadiz host gill tissue clone Mer
GQ106875.1 gg_id:435090 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw542a0
GQ114179.1 gg_id:393759 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
AF078760.1 gg_id:7052 Acidovorax konjaci str. ATCC 33996
AB076844.1 gg_id:28959 Acidovorax sp. str. OS-6
GQ098446.1 gg_id:400311 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw559g
GQ099609.1 gg_id:451960 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
AY837725.1 gg_id:141709 -Based Identification Midgut Field-Caught Anopheles gambiae Sensu Lato and . funes
EU104224.1 gg_id:356016 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ114282.1 gg_id:422535 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
EU434475.1 gg_id:275733 Acidovorax defluvii str. b268
GQ099219.1 gg_id:447125 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ102686.1 gg_id:413906 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ497649.1 gg_id:585668 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
GQ104106.1 gg_id:447512 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw563c0
AF015487.1 gg_id:7077 Pseudomonas sp. str. P51
FJ658868.1 gg_id:568875 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
FJ477624.1 gg_id:552067 gut symbionts are tightly linked herbivory ants whole extracted single ant clone UAB-
FJ477611.1 gg_id:578828 gut symbionts are tightly linked herbivory ants whole extracted mid- and hind-gut sin
AF508114.1 gg_id:66230 Acidovorax avenae C1
FJ657748.1 gg_id:545408 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte

NR_028973.1	584295	9153.6	5046.4	12486.3	9774.4	2608.7	6126.0
CU466871.1	339277	8586.1	3645.1	12308.0	13942.3	1674.1	4698.5
FJ593725.1	531432	7959.7	5238.3	12992.7	10697.8	3505.5	7237.2
AY093698.1	55345	3483.6	3680.9	12540.3	7469.2	1328.8	3883.4
GQ091955.1	414179	14860.9	7335.2	16067.9	14515.6	8408.6	10038.8
AB269774.1	208383	3633.7	2919.7	5796.3	7448.0	1241.8	3786.3
GQ107139.1	397297	16649.7	8241.0	15923.9	17006.6	5395.8	9754.0
EU202950.1	251020	8126.2	3485.3	8023.8	11636.0	1818.9	4717.1
GQ102018.1	387956	5945.3	2898.1	7863.1	11115.5	1530.0	2869.0
DQ264575.1	143236	10531.9	5663.3	14245.6	13640.5	5508.8	7298.8
AJ400840.1	74685	7700.7	2542.1	9050.8	8391.7	1815.5	4587.4
AB008429.1	7063	10785.6	7162.9	14462.6	15812.3	2087.6	5694.0
AB167175.1	107894	5293.9	2096.0	3200.0	4184.9	2060.7	4335.9
GQ107342.1	440564	13277.3	6208.1	11856.4	15272.9	3501.8	7427.9
AF078762.1	7047	4746.9	2630.9	12784.2	7935.4	1562.8	2719.6
GQ068971.1	447274	14963.2	11769.4	14897.7	18775.5	12290.2	11016.8
DQ264434.1	141042	12960.5	7183.5	7512.3	12604.4	7250.7	8105.0
FJ560467.1	546272	11805.6	5561.5	12579.7	13175.5	4010.6	6720.1
AM084008.1	140621	13605.3	6699.9	12426.1	15790.8	4550.7	8100.2
GQ022385.1	487284	13587.2	7880.1	10114.2	14667.8	6314.3	9269.5
FM213427.1	327583	8534.9	6931.5	9414.2	12421.6	7378.9	9028.4
GQ106875.1	435090	10201.5	4765.7	9468.2	12123.0	2883.7	6655.3
GQ114179.1	393759	8354.3	5054.4	7530.6	7727.8	4185.6	6503.2
AF078760.1	7052	1889.3	1563.5	9752.4	8924.0	671.4	1858.2
AB076844.1	28959	12627.3	4479.4	7793.4	12160.8	5404.5	8064.5
GQ098446.1	400311	10395.9	6417.8	10332.4	11566.8	5344.2	8357.6
GQ099609.1	451960	14664.2	6878.4	15467.7	17062.6	3902.4	8648.2
AY837725.1	141709	10069.9	6779.6	10297.7	8902.9	6924.2	7484.3
EU104224.1	356016	8061.5	2930.4	9265.5	10268.5	1672.9	7033.0
GQ114282.1	422535	13921.3	6952.8	15178.9	15546.7	4019.1	9012.9
EU434475.1	275733	7761.5	3265.7	7155.3	8670.2	2275.1	6706.9
GQ099219.1	447125	13971.2	8708.0	6759.5	13123.7	7011.5	10513.3
GQ102686.1	413906	15312.7	7712.1	16265.8	16912.0	4169.9	8481.8
FJ497649.1	585668	5860.5	5133.0	3762.1	7054.8	3087.7	4279.4
GQ104106.1	447512	11462.1	5510.2	7722.6	12900.3	6422.6	9166.9
AF015487.1	7077	7662.9	3117.4	5368.0	8040.5	1536.3	3281.7
FJ658868.1	568875	6768.7	4310.8	10367.5	8846.8	2763.9	5094.0
FJ477624.1	552067	5093.0	3783.7	7152.5	9658.0	3671.0	5656.7
FJ477611.1	578828	8488.7	9444.7	7254.6	9513.4	9859.5	10202.2
AF508114.1	66230	6047.5	1530.4	4255.3	4362.1	1889.8	2829.9
FJ657748.1	545408	6812.6	6449.1	4336.5	7599.7	7776.3	6420.5

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s__Comamonas denitrificans	16150
s__Comamonas denitrificans	16295

FJ658799.1 gg_id:510766 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
FJ658952.1 gg_id:553262 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
FJ658390.1 gg_id:544123 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
AB120964.1 gg_id:99037 Aquamonas fontana str. AQ10
DQ640723.1 gg_id:227889 full-scale EBPR sludge clone Skagen135
AF526926.2 gg_id:62982 Mars Odyssey Orbiter and encapsulation facility clone T5-4 sp.
AY133071.1 gg_id:56377 TCE-contaminated site clone ccs221
DQ521541.1 gg_id:193826 Antarctic lake ice cover clone ANTLV7_G03
AY662013.1 gg_id:137452 uranium-contaminated groundwater clone 015C-G04
AF526920.2 gg_id:62991 Mars Odyssey Orbiter and encapsulation facility clone T8-7 sp.
EU150266.1 gg_id:279514 acidobacteria and soil Niwot Ridge LTER clone Ni_F8P2
NR_028713.1 gg_id:585432 Curvibacter delicatus str. 146; LMG 4328
D14320.1 gg_id:6938 Brachymonas denitrificans str. -P1
EU434344.1 gg_id:271636 Brachymonas denitrificans str. a265
EU434398.1 gg_id:265311 Brachymonas denitrificans str. a310
AB286490.1 gg_id:208338 Reducing production and domination comamonadaceae reducing oxygen supply was
AJ318129.1 gg_id:21007 Waste-gas biofilter clone BIfdi44
AM420229.1 gg_id:239064 Noma subgingival plaque clone 601H06(oral)
FJ982927.1 gg_id:460813 Comamonas sp. str. ST18
AB164432.1 gg_id:103333 Comamonas badia str. IAM 14839
AJ576357.1 gg_id:107318 hindgut homogenate Pachnoda ephippiata larva clone PeH41
AF234720.1 gg_id:73090 sludge clone A6b
EU346912.1 gg_id:265983 Brachymonas sp. str. AImA4
AB286456.1 gg_id:216049 Reducing production and domination comamonadaceae reducing oxygen supply was
FJ959768.1 gg_id:584835 bottlenose dolphin upper respiratory tract blowhole clone D8A8_102
AB286474.1 gg_id:214136 Reducing production and domination comamonadaceae reducing oxygen supply was
EU881354.1 gg_id:306436 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
AB286506.1 gg_id:211133 Reducing production and domination comamonadaceae reducing oxygen supply was
GQ010546.1 gg_id:499118 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ110427.1 gg_id:447775 Topographical and Temporal Human Skin Microbiome skin back clone nbw659e10c1
AM283038.1 gg_id:159681 Caldimonas sp. str. Han85
EU024140.1 gg_id:247295 Comamonas aquatica str. CIP 107986
EU464974.1 gg_id:295063 African elephant feces clone AFYEL_aaj66a08
DQ854969.1 gg_id:161904 Comamonas sp. str. GPTSA5
EU464791.1 gg_id:289604 Hartmann's mountain zebra feces clone AFZEB_aaj70h03
AF408327.1 gg_id:36914 Comamonas sp. clone KL-11-1-9
EU841519.1 gg_id:337127 Comamonas aquatica str. 406
DQ824524.1 gg_id:188323 human fecal clone RL185_aaj69c02
AJ430344.1 gg_id:73664 Comamonas aquatica str. LMG 2370
AF233878.1 gg_id:40166 Comamonas denitrificans str. 2.99g
AF233879.1 gg_id:74723 Comamonas denitrificans str. 5.38g

FJ658799.1	510766	12110.1	11810.0	10365.2	11440.7	13790.3	11418.4
FJ658952.1	553262	6766.0	2793.2	5388.0	6683.7	994.9	3629.3
FJ658390.1	544123	6451.9	6029.7	6700.9	7961.9	4586.1	5564.7
AB120964.1	99037	6894.1	3853.6	11672.5	9719.2	2091.8	3869.2
DQ640723.1	227889	7163.2	5510.5	13140.0	12861.3	5074.6	4285.8
AF526926.2	62982	9252.5	8130.7	13821.6	11855.4	10085.3	9598.1
AY133071.1	56377	9008.7	3863.3	14225.4	11568.4	2853.1	5110.4
DQ521541.1	193826	9252.8	4168.4	14301.3	13446.5	2791.5	5546.3
AY662013.1	137452	9646.2	5411.0	11981.4	11861.0	3760.1	8114.9
AF526920.2	62991	8917.3	5581.4	3909.2	9999.6	7488.6	7041.2
EU150266.1	279514	9561.6	6454.5	14577.6	9001.7	5723.6	4862.1
NR_028713.1	585432	6748.1	3234.0	16298.6	12916.2	1366.9	2851.4
D14320.1	6938	12801.7	11831.7	16791.4	15243.5	11589.3	11787.3
EU434344.1	271636	6097.4	4691.4	8818.3	8860.6	3718.5	6969.1
EU434398.1	265311	3766.3	2337.9	5171.2	5816.9	4081.6	6821.1
AB286490.1	208338	6546.0	4429.0	6212.3	9852.0	3590.6	6754.8
AJ318129.1	21007	4298.4	4614.2	6509.7	5729.9	2054.4	5523.2
AM420229.1	239064	10783.3	9051.8	8698.6	11716.9	7151.6	11144.4
FJ982927.1	460813	3730.3	6509.8	8292.2	6764.9	5775.8	6730.2
AB164432.1	103333	1811.2	1720.2	2380.8	2533.6	655.0	929.5
AJ576357.1	107318	2724.2	642.1	846.3	2744.9	1023.3	839.1
AF234720.1	73090	3521.7	2207.2	5996.2	5249.2	2340.9	3129.5
EU346912.1	265983	4906.0	4515.3	3299.3	7834.3	8216.1	7157.4
AB286456.1	216049	14577.6	11430.4	14022.7	14895.6	11879.8	13308.7
FJ959768.1	584835	3333.7	2652.4	6199.6	7802.6	3551.7	4687.2
AB286474.1	214136	8201.6	7269.7	8294.3	11322.6	7549.7	8390.4
EU881354.1	306436	7281.3	3495.9	5242.0	7483.8	3705.8	5872.3
AB286506.1	211133	8361.7	6329.0	5508.2	9231.6	4571.3	6964.2
GQ010546.1	499118	4234.0	2338.3	6180.6	6147.7	2792.9	3624.2
GQ110427.1	447775	12546.9	10979.5	11575.4	9876.4	7664.4	10207.2
AM283038.1	159681	3190.7	2547.7	4596.2	3596.4	2180.8	5075.1
EU024140.1	247295	14666.1	12589.2	14392.3	14963.7	7664.5	9814.3
EU464974.1	295063	6040.7	2531.9	6255.3	5375.2	3341.5	4084.9
DQ854969.1	161904	6947.0	2993.8	8437.3	5857.0	3382.0	5101.6
EU464791.1	289604	10868.2	6422.2	19300.3	13370.0	8863.2	8222.6
AF408327.1	36914	11410.7	4471.4	11629.8	9614.5	2513.9	4875.0
EU841519.1	337127	11004.1	3641.6	11308.4	7993.0	2259.9	4695.5
DQ824524.1	188323	11687.5	6913.0	20624.0	14607.8	8482.1	7482.6
AJ430344.1	73664	15911.8	14277.6	11830.7	16552.7	9608.9	12364.1
AF233878.1	40166	4242.7	3413.2	6510.2	6327.6	2899.4	4124.7
AF233879.1	74723	4478.3	3804.5	6300.9	7372.3	3541.2	4974.6

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s__Comamonas kerstersii	16946
s__Comamonas terrigena	16026
s__Comamonas terrigena	16074
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AF233877.1 gg_id:23191 Comamonas denitrificans str. 123
AJ430348.1 gg_id:66684 Comamonas kerstersii str. LMG 5323
AB021418.1 gg_id:6936 Comamonas terrigena str. IAM 12052T
AJ430343.1 gg_id:66690 Comamonas terrigena str. LMG 1249
AJ420326.1 gg_id:17652 Comamonas terrigena str. DSM 7099
EU024142.1 gg_id:240089 Comamonas terrigena str. LMG 5520
AM184229.1 gg_id:160747 Comamonas terrigena str. WAB1888
NR_028719.1 gg_id:545968 Comamonas terrigena str. IMI 359870; ATCC 8461
EU337122.1 gg_id:545663 Comamonas denitrificans str. 2B7
GU454930.1 gg_id:524752 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
DQ824755.1 gg_id:189547 human fecal clone RL185_aaj72g08
EU465136.1 gg_id:290700 African elephant feces clone AFYEL_aaj68e11
FJ658617.1 gg_id:509630 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
EU464722.1 gg_id:300641 Hartmann's mountain zebra feces clone AFZEB_aaj69f11
AY566581.1 gg_id:108740 Comamonas sp. str. PG-08
GQ179675.1 gg_id:465713 Heterogeneity vaginal microbial within individuals vagina clone VE3A04
EU465091.1 gg_id:291187 African elephant feces clone AFYEL_aaj67h12
EU465027.1 gg_id:296452 African elephant feces clone AFYEL_aaj66h05
EU536017.1 gg_id:286592 profile human microbiota antecubital fossa (inner elbow) skin clone nbt161h12
EU465029.1 gg_id:292604 African elephant feces clone AFYEL_aaj66h08
EU465048.1 gg_id:302343 African elephant feces clone AFYEL_aaj67c02
EU465099.1 gg_id:302440 African elephant feces clone AFYEL_aaj68a11
AY635871.1 gg_id:99471 Comamonas sp. str. BM-9_6
EU464843.1 gg_id:295086 Hartmann's mountain zebra feces clone AFZEB_aaj71g07
EU465006.1 gg_id:293491 African elephant feces clone AFYEL_aaj66e11
EU771834.1 gg_id:310863 African elephant feces clone AFYEL_aaj65h12
AB076865.1 gg_id:42211 anaerobic sludge clone OS1L-7
EU771819.1 gg_id:310322 African elephant feces clone AFYEL_aaj68f04
EU464881.1 gg_id:301051 Hartmann's mountain zebra feces clone AFZEB_aaj72d04
EU465050.1 gg_id:287469 African elephant feces clone AFYEL_aaj67c06
AY856846.1 gg_id:111198 Comamonas sp. str. 46
EU464826.1 gg_id:287428 Hartmann's mountain zebra feces clone AFZEB_aaj71e07
GQ389171.1 gg_id:571114 quality deterioration drinking system during serious red water outbreak clone D40
EU771661.1 gg_id:334294 African elephant feces clone AFEL_aai29g11
EU464941.1 gg_id:302302 African elephant feces clone AFYEL_aaj65e07
EU465157.1 gg_id:292068 African elephant feces clone AFYEL_aaj68h04
EU465046.1 gg_id:299793 African elephant feces clone AFYEL_aaj67b12
EU464997.1 gg_id:294410 African elephant feces clone AFYEL_aaj66d12
EU465004.1 gg_id:294874 African elephant feces clone AFYEL_aaj66e08
EU465015.1 gg_id:298465 African elephant feces clone AFYEL_aaj66f12
DQ453128.1 gg_id:156701 Comamonas sp. str. Dant 3-8

AF233877.1	23191	2471.1	2623.3	4800.2	5250.2	2965.8	3311.8
AJ430348.1	66684	17359.1	5929.1	19759.6	16536.7	5360.6	7927.3
AB021418.1	6936	14089.7	8876.6	19569.1	18185.1	9637.8	11106.4
AJ430343.1	66690	9203.6	5309.7	10163.8	8018.0	3251.6	5685.0
AJ420326.1	17652	9895.4	6384.3	11819.1	8919.9	5097.1	7686.6
EU024142.1	240089	8555.4	5246.4	10034.4	7888.7	3387.3	5913.1
AM184229.1	160747	10421.9	9258.6	17742.1	11263.9	7351.7	8317.6
NR_028719.1	545968	10192.8	7574.7	17234.2	11995.5	6718.6	8189.7
EU337122.1	545663	6128.8	4968.9	6688.8	7066.0	3835.0	5886.0
GU454930.1	524752	4876.3	3658.6	7561.2	6467.0	2891.6	4375.6
DQ824755.1	189547	9795.5	7168.9	13611.1	10331.1	7444.4	8476.8
EU465136.1	290700	8999.8	6317.9	5629.3	10152.3	7300.8	6201.8
FJ658617.1	509630	9224.9	5633.9	11062.8	11296.7	5084.4	4922.1
EU464722.1	300641	12486.5	8403.7	15114.1	13222.8	9112.2	10804.6
AY566581.1	108740	17084.7	13013.2	12106.3	15219.3	11723.5	12407.1
GQ179675.1	465713	6008.0	850.6	3727.4	4561.2	552.2	2049.4
EU465091.1	291187	10770.2	5666.2	13040.3	10379.4	4366.2	5973.1
EU465027.1	296452	5636.2	2684.1	9553.4	8938.3	2874.6	6118.1
EU536017.1	286592	11753.6	6072.6	13032.7	10692.7	3995.7	7143.7
EU465029.1	292604	8672.3	5395.6	15549.4	11859.1	4996.4	4191.2
EU465048.1	302343	3030.7	1972.7	5003.1	5548.5	1521.1	2747.7
EU465099.1	302440	7542.4	4538.4	10476.2	9473.8	4988.9	7794.4
AY635871.1	99471	13127.1	4638.0	16661.6	11591.0	4323.0	6778.2
EU464843.1	295086	9045.9	3840.0	11893.3	11498.4	3075.1	2939.3
EU465006.1	293491	5797.5	5222.1	8406.3	7293.3	10074.4	7428.2
EU771834.1	310863	4311.3	4092.4	3974.5	6631.3	8184.4	7044.1
AB076865.1	42211	3260.9	2099.4	4325.9	5161.0	1366.8	2934.9
EU771819.1	310322	11032.2	5712.8	11758.5	13003.9	6241.4	6119.4
EU464881.1	301051	12474.2	14451.5	10770.4	12937.8	13884.4	12365.5
EU465050.1	287469	7746.0	4228.1	15374.1	10136.4	4174.8	6755.8
AY856846.1	111198	10824.0	10545.3	12083.7	12860.4	10588.3	10306.9
EU464826.1	287428	3529.8	3284.1	8143.6	6054.5	3569.2	3967.7
GQ389171.1	571114	10739.4	4738.9	6781.2	9346.2	5722.6	6409.5
EU771661.1	334294	5083.2	3505.7	5676.8	6412.4	3321.0	3905.5
EU464941.1	302302	7478.2	5730.0	2555.7	6948.4	3577.2	3414.6
EU465157.1	292068	3241.9	2599.7	3453.9	5981.3	2978.9	1718.0
EU465046.1	299793	12298.5	9014.8	12600.1	12861.0	7760.7	7174.3
EU464997.1	294410	10525.6	10384.9	9434.0	10504.1	10430.5	8347.3
EU465004.1	294874	3803.5	3042.4	2461.9	7836.2	1647.2	1501.1
EU465015.1	298465	15220.2	14505.5	7678.6	11093.7	13510.5	12800.2
DQ453128.1	156701	5063.1	3230.6	7176.6	7089.0	5031.7	4598.1

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EU464943.1 gg_id:299547 African elephant feces clone AFYEL_aaj65e11
EF114434.1 gg_id:534604 strains recovered during surveys Burkholderia pseudomallei northern Australia rod
EF565937.1 gg_id:228582 Comamonas sp. str. NF27
EU465126.1 gg_id:287764 African elephant feces clone AFYEL_aaj68d09
AF501880.1 gg_id:71872 Comamonas testosteroni str. SMCC B0589
EU467917.1 gg_id:289291 cheetah feces clone CE2_a08
GU454975.1 gg_id:515113 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
EU468077.1 gg_id:291421 cheetah feces clone CE2_d08_3
EU464621.1 gg_id:289827 African elephant feces clone AFEL_aai32a05
AY291591.1 gg_id:87769 Comamonas testosteroni str. CNB1
AY134850.1 gg_id:58604 Comamonas sp. str. SFCD1
EU464754.1 gg_id:291460 Hartmann's mountain zebra feces clone AFZEB_aaj70c03
EU468035.1 gg_id:297644 cheetah feces clone CE2_f06_1
EU464969.1 gg_id:298206 African elephant feces clone AFYEL_aaj66a02
EU464920.1 gg_id:299963 African elephant feces clone AFYEL_aaj65b11
AY819705.1 gg_id:109404 Comamonas sp. str. JS46
AJ606336.1 gg_id:101448 Comamonas testosteroni SB4
EU464815.1 gg_id:287989 Hartmann's mountain zebra feces clone AFZEB_aaj71c10
EU465125.1 gg_id:298220 African elephant feces clone AFYEL_aaj68d08
EU464514.1 gg_id:302159 African elephant feces clone AFEL_aai30d10
EU779419.1 gg_id:343489 Hartmann's Mountain Zebra feces clone AFZEB_aaj72d07
EU464929.1 gg_id:294023 African elephant feces clone AFYEL_aaj65c11
EF515707.1 gg_id:225977 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
GQ008024.1 gg_id:501642 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
EU464698.1 gg_id:298530 Hartmann's mountain zebra feces clone AFZEB_aaj69d04
EU464986.1 gg_id:294420 African elephant feces clone AFYEL_aaj66c06
EU537205.1 gg_id:281659 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68d07
FJ893904.1 gg_id:540808 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
AF532869.1 gg_id:91652 Comamonas sp. str. D1
EU464891.1 gg_id:300806 Hartmann's mountain zebra feces clone AFZEB_aaj72f06
EU464935.1 gg_id:293225 African elephant feces clone AFYEL_aaj65d12
EU464774.1 gg_id:288302 Hartmann's mountain zebra feces clone AFZEB_aaj70e07
EU465010.1 gg_id:298312 African elephant feces clone AFYEL_aaj66f07
EU464915.1 gg_id:291947 African elephant feces clone AFYEL_aaj65a11
AJ251577.1 gg_id:38824 Comamonas nitrativorans str. 23310
AF233876.1 gg_id:18248 Comamonas denitrificans str. 110
EU465109.1 gg_id:287376 African elephant feces clone AFYEL_aaj68b09
EU465146.1 gg_id:297240 African elephant feces clone AFYEL_aaj68g02
EU536192.1 gg_id:282831 profile human microbiota antecubital fossa (inner elbow) skin clone nbt12g10
AB109889.1 gg_id:106408 Curvibacter gracilis str. 7-1
DQ001153.1 gg_id:118400 Rhodobacter sphaeroides str. Il106

EU464943.1	299547	14189.5	7831.1	11202.2	11570.1	8302.5	9223.4
EF114434.1	534604	5874.4	1451.2	5122.0	6242.3	2277.6	3473.9
EF565937.1	228582	14739.0	9065.1	12816.6	13920.5	10315.1	9783.9
EU465126.1	287764	12496.3	10928.8	7313.4	12610.7	9328.2	10990.5
AF501880.1	71872	1911.7	517.1	8766.9	6822.7	162.1	259.2
EU467917.1	289291	8597.3	4345.7	9390.6	7802.3	4631.4	4804.6
GU454975.1	515113	12814.8	9943.3	13090.8	12811.8	7919.2	9965.7
EU468077.1	291421	15306.6	8608.7	15888.4	9940.0	10399.6	10355.8
EU464621.1	289827	16028.1	7940.7	12838.3	12175.0	7080.3	8554.8
AY291591.1	87769	11198.6	8927.5	6155.5	11413.0	11492.5	10273.6
AY134850.1	58604	7270.6	4248.5	12516.6	9217.1	3695.9	4950.0
EU464754.1	291460	13353.9	9675.2	11606.8	13005.1	6294.1	9007.2
EU468035.1	297644	11146.2	3654.8	16397.7	9411.6	4053.4	5862.3
EU464969.1	298206	7210.3	5045.2	14648.7	8380.5	4292.3	4006.5
EU464920.1	299963	7304.2	5975.8	12606.7	9081.6	5851.9	5836.2
AY819705.1	109404	7920.1	4090.6	10873.1	7605.6	5160.9	5758.5
AJ606336.1	101448	5724.8	1819.3	6240.1	4502.5	1830.5	2412.8
EU464815.1	287989	15607.0	13533.5	19518.2	15751.2	15761.7	12557.4
EU465125.1	298220	11870.0	8008.1	13728.4	12084.7	8523.7	9233.6
EU464514.1	302159	8740.0	5267.7	12142.7	10501.5	4264.5	4513.7
EU779419.1	343489	14732.8	13575.4	17499.4	16180.0	15031.9	13749.1
EU464929.1	294023	8849.8	2131.2	8675.7	5371.2	2341.8	4148.9
EF515707.1	225977	11216.6	6949.1	11884.1	8317.8	5870.1	5142.4
GQ008024.1	501642	2200.4	3231.0	3451.6	2069.3	2476.8	2761.1
EU464698.1	298530	10591.4	8176.4	9561.6	12359.5	6474.4	7778.9
EU464986.1	294420	4968.6	2599.2	6681.2	7267.5	3654.7	1548.8
EU537205.1	281659	15472.6	10546.8	5618.2	11152.0	8426.4	8903.4
FJ893904.1	540808	1306.6	1357.6	5029.9	3154.7	2741.2	1630.0
AF532869.1	91652	17360.1	6930.5	15717.8	14662.9	4368.6	8203.9
EU464891.1	300806	5186.9	2571.7	10032.7	5575.2	4166.4	4234.7
EU464935.1	293225	13074.9	12130.1	8336.9	12158.2	13230.1	11768.5
EU464774.1	288302	5953.5	2808.1	7950.0	8107.1	2294.8	2900.2
EU465010.1	298312	7853.3	6506.4	12738.9	11126.6	7932.0	6749.3
EU464915.1	291947	11801.1	9629.0	18230.5	13455.9	9927.5	8666.4
AJ251577.1	38824	10091.1	7934.3	14043.0	10886.6	6740.4	8068.2
AF233876.1	18248	9513.1	4689.1	10184.3	11017.1	4573.8	6334.8
EU465109.1	287376	5213.5	3818.0	8033.7	6679.3	4596.6	5809.5
EU465146.1	297240	11397.2	9110.5	12002.1	12929.5	12193.7	11950.8
EU536192.1	282831	8903.6	7339.0	14598.0	10235.8	6778.0	7838.4
AB109889.1	106408	12150.9	7679.8	14418.8	14414.2	5033.7	7159.7
DQ001153.1	118400	13312.4	9252.0	13078.2	12263.0	9018.6	10716.8

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AF078774.1 gg_id:6901 Delftia acidovorans str. ACM 489
AY899912.1 gg_id:111999 Delftia tsuruhatensis str. AD9
AB361589.1 gg_id:269063 Delftia acidovorans str. 182
AY367007.1 gg_id:93731 Delftia acidovorans Eh2-1
GQ466172.1 gg_id:561105 Delftia acidovorans str. CC
AB021417.1 gg_id:6904 Delftia acidovorans str. IAM 12409T
AY753653.1 gg_id:98977 Delftia acidovorans str. VH240351
GQ102837.1 gg_id:389963 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ008220.1 gg_id:501445 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ105301.1 gg_id:410258 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ008842.1 gg_id:500824 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ032647.1 gg_id:399312 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu544a11
GQ103597.1 gg_id:411332 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ092967.1 gg_id:407300 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407d07
GQ092182.1 gg_id:461603 Topographical and Temporal Human Skin Microbiome skin palm clone nbw409c04c1
GQ092800.1 gg_id:373771 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
GQ076386.1 gg_id:434625 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
GQ023982.1 gg_id:485687 Topographical and Temporal Human Skin Microbiome skin palm clone nbw124g04c1
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GQ050988.1 gg_id:456428 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ037723.1 gg_id:439669 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
GQ103559.1 gg_id:460694 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ033378.1 gg_id:386659 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ038138.1 gg_id:435479 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu38
GQ113657.1 gg_id:388046 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ092291.1 gg_id:466839 Topographical and Temporal Human Skin Microbiome skin palm clone nbw412c06c1
EU342380.2 gg_id:273203 Diaphorobacter oryzae str. RF21
GQ102386.1 gg_id:389937 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ095327.1 gg_id:456937 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ047914.1 gg_id:386775 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139a04c1
GQ105323.1 gg_id:410282 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
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GQ102373.1 gg_id:414490 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ060251.1 gg_id:448700 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ111713.1 gg_id:422649 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ108916.1 gg_id:455943 Topographical and Temporal Human Skin Microbiome skin palm clone nbw719d01c
GQ047976.1 gg_id:466590 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g09c1
GQ115549.1 gg_id:462734 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687d0
GQ037192.1 gg_id:419037 Topographical and Temporal Human Skin Microbiome skin palm clone nbu390a04c1

AB231159.1	145870	17638.0	11709.3	11790.7	17415.8	13082.5	14503.2
AF078774.1	6901	13035.6	5813.5	15582.4	14641.2	3354.0	5701.8
AY899912.1	111999	12203.3	6295.5	9007.6	12470.7	6193.9	9033.8
AB361589.1	269063	13233.1	7547.7	10705.7	12323.0	8353.7	10490.5
AY367007.1	93731	11169.9	6910.8	11954.3	11563.5	4245.0	6176.9
GQ466172.1	561105	20152.0	13919.3	22018.3	19264.3	13534.4	13996.4
AB021417.1	6904	13931.3	7482.2	14689.3	14202.6	7392.6	9384.5
AY753653.1	98977	9911.8	4681.1	8250.2	11088.3	5740.9	6664.2
GQ102837.1	389963	9904.6	3434.7	9267.0	9108.6	3428.8	5771.9
GQ008220.1	501445	5966.5	2454.7	8466.5	7496.5	2586.8	4925.9
GQ105301.1	410258	8276.8	4924.6	7417.1	6719.6	3981.7	5013.0
GQ008842.1	500824	7656.7	4725.7	11587.2	9687.9	3361.0	6324.4
GQ032647.1	399312	9241.2	5007.3	14902.7	11520.7	4846.4	5947.0
GQ103597.1	411332	8126.2	5978.7	6495.3	9709.2	11654.6	10017.9
GQ092967.1	407300	12500.3	7521.5	15005.9	14318.5	5813.1	9360.7
GQ092182.1	461603	11309.5	9146.7	8958.4	11428.4	6736.5	9640.5
GQ092800.1	373771	20236.3	15228.9	16544.2	19364.1	14367.8	14354.5
GQ076386.1	434625	4521.8	3055.5	4509.6	6142.6	2482.0	3981.2
GQ023982.1	485687	7977.4	5900.7	12294.4	10122.6	5049.6	7040.5
GQ023094.1	486575	13771.0	10112.5	6960.2	15018.8	14379.6	13757.5
GQ089285.1	455798	13318.8	5947.6	9389.6	11242.6	5157.6	6852.1
GQ050988.1	456428	14373.7	10021.7	16968.7	17726.6	14169.9	14969.6
GQ037723.1	439669	11795.4	14884.4	11240.8	11162.6	9431.1	10085.9
GQ103559.1	460694	8500.1	4798.5	9094.8	8318.4	4793.5	6288.9
GQ033378.1	386659	10566.6	5808.3	13534.3	12452.6	6537.0	7775.6
GQ038138.1	435479	9424.6	3094.3	10355.4	8867.4	3419.1	5203.4
GQ113657.1	388046	12017.8	6787.6	11058.3	13166.8	6688.4	9045.1
GQ092291.1	466839	15859.1	8833.4	11223.8	17759.2	8743.2	8348.0
EU342380.2	273203	5224.1	2070.0	8903.2	5606.6	1157.6	2279.9
GQ102386.1	389937	8803.1	2795.5	7292.7	8799.2	2368.1	4020.8
GQ095327.1	456937	9583.0	6075.2	7612.2	9916.0	2951.5	5080.5
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GQ062975.1	441174	11044.9	5261.0	11009.8	12632.2	6027.5	7939.0
GQ102373.1	414490	11653.3	9698.0	11633.3	13777.8	13158.8	12715.7
GQ060251.1	448700	10339.0	4358.2	11566.5	11583.2	4456.5	6779.3
GQ111713.1	422649	11261.9	4915.1	8189.0	12160.8	3533.3	8589.9
GQ108916.1	455943	11567.5	4537.5	13351.8	12251.4	4509.1	6861.3
GQ047976.1	466590	11091.8	4946.4	11566.7	10262.5	6058.1	7841.8
GQ115549.1	462734	9264.8	8642.2	13467.4	12683.5	10349.2	10030.4
GQ037192.1	419037	3613.8	2642.0	9090.3	6605.0	2624.5	4199.9

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GQ105405.1 gg_id:429340 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ023025.1 gg_id:486644 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ087317.1 gg_id:377148 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ096026.1 gg_id:434741 Topographical and Temporal Human Skin Microbiome skin back clone nbw385e12c1
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GQ062384.1 gg_id:444810 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ105194.1 gg_id:435980 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ088002.1	432420	20740.1	16690.5	13338.9	15841.1	15415.9	15068.7
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GQ002346.1	507316	12070.6	7468.5	12249.8	12940.0	5527.7	7662.5
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GQ060027.1	386825	9962.7	3630.5	9593.6	9490.5	3679.3	5893.6
GQ115763.1	403748	5805.0	2951.1	9345.0	7497.5	3549.8	5102.4
GQ084891.1	374735	5970.1	3076.7	7635.2	8475.4	4006.3	5916.7
GQ115756.1	464070	21858.0	19112.2	15485.4	18759.8	19386.7	17795.9
GQ115254.1	384598	15076.8	11680.3	16585.5	18166.2	12704.2	14236.6
GQ022055.1	487613	22352.7	18446.2	16806.5	20375.1	18057.1	17751.9
GQ038675.1	433955	10824.0	4396.2	10800.9	10151.1	5177.7	7024.2
GQ094473.1	453678	11424.0	5220.7	13405.8	11602.4	5092.4	7256.9
GQ033109.1	464483	11825.8	6239.6	16673.7	13530.7	7562.4	10953.9
GQ075532.1	436249	10403.7	5672.3	13330.1	10549.2	4004.7	7380.1
GQ070548.1	439936	9818.7	4353.9	12372.2	10994.4	3204.7	6891.6
GQ098172.1	439954	12939.4	8694.1	15772.3	14933.6	11657.7	12289.2
GQ115938.1	419686	10991.1	4704.2	10065.9	9697.9	5017.6	6929.2
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GQ024900.1	484770	8241.7	3073.0	8298.6	8169.8	3401.2	5906.3
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GQ105405.1	429340	9391.6	5130.9	7796.6	10506.4	4744.6	7090.1
GQ023025.1	486644	9236.3	5599.5	6273.9	8409.9	4277.1	6649.2
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GQ022695.1 gg_id:486975 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ008349.1 gg_id:501316 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ023731.1 gg_id:485935 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ021761.1 gg_id:487908 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ045522.1 gg_id:466285 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
GQ083081.1 gg_id:414741 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ023923.1 gg_id:485746 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ015141.1 gg_id:494526 Topographical and Temporal Human Skin Microbiome skin palm clone nbw764h09c

GQ074986.1	451221	9998.6	4854.4	10538.1	9665.2	5660.6	7310.0
DQ988255.1	196892	10269.6	5769.7	11697.6	10148.5	4268.9	6514.8
GQ022695.1	486975	10285.6	5460.9	11021.8	12630.0	5362.3	8035.9
GQ008349.1	501316	10531.3	6866.7	13724.2	10796.7	4658.7	6264.4
GQ083533.1	458677	7803.6	5571.7	6395.1	9584.8	6475.5	6816.4
GQ107072.1	432134	9046.7	4477.7	10115.2	11165.8	4012.4	6372.3
GQ022092.1	487576	11626.8	5311.5	19915.8	12233.0	7879.7	7977.4
GQ023888.1	485781	8722.3	3792.6	7381.4	8238.1	4106.5	5930.1
GQ103014.1	443883	12574.2	6269.5	11222.3	12008.4	4092.1	6540.2
GQ089299.1	448221	7244.3	4161.9	11244.2	9426.4	2714.5	6126.5
GQ022022.1	487645	10410.7	4279.2	12356.4	10063.5	4253.9	6985.1
GQ023045.1	486624	18688.7	17699.9	13482.3	17166.7	17150.0	17336.7
GQ108814.1	465031	10886.3	8739.7	8471.4	10081.3	6430.1	6923.2
GQ070084.1	407790	10112.2	5174.0	9378.2	9516.9	4209.1	5313.9
GQ115334.1	440345	14375.2	10976.1	9757.9	15050.5	13954.0	11928.2
GQ065252.1	455893	8777.1	2994.3	10756.3	8417.7	4159.7	5632.0
GQ106640.1	412540	7940.4	5021.7	8071.2	8929.4	5557.7	7420.0
GQ024723.1	484948	10301.4	3899.0	12158.3	10277.6	3787.7	6137.1
GQ038841.1	457407	12110.5	7545.5	9055.1	11665.6	8416.4	8649.7
GQ096807.1	392240	12413.8	7183.7	6303.5	14776.3	8621.0	8628.3
GQ102406.1	415075	8765.5	2929.0	9657.7	8725.1	4151.6	5684.1
GQ115305.1	433808	12956.4	7523.7	10676.4	14185.2	12042.3	11129.7
GQ096025.1	379464	7490.5	2947.6	5519.4	6849.4	2455.2	4398.2
GQ008069.1	501596	10878.0	4878.7	12954.9	10783.2	4939.7	7063.3
GQ112122.1	387746	14933.8	10680.6	14209.4	15676.5	12150.8	10888.0
GQ023417.1	486252	8208.0	2822.3	7293.4	8511.1	3324.8	5665.9
GQ037440.1	458162	9241.1	3589.5	8329.7	10972.2	3729.8	5114.8
GQ021046.1	488622	14549.2	13113.8	11735.9	16400.8	14610.4	13529.9
GQ038903.1	377128	10483.5	4876.7	10557.5	10205.0	3797.3	6109.8
GQ058999.1	374074	10704.2	6018.9	13250.7	12168.4	4505.9	7822.7
GQ035860.1	416831	16081.5	9533.2	10913.8	17949.4	5351.6	7651.3
GQ091716.1	448179	12892.2	5423.3	14230.3	13766.1	4743.1	8722.0
GQ007643.1	502021	9679.6	5928.9	10494.8	12859.2	4904.2	7305.9
GQ039247.1	394725	25400.0	22187.4	19135.9	22429.0	23107.4	20459.5
GQ093458.1	461748	10248.7	4319.6	12071.8	12237.8	3197.8	6947.9
GQ023731.1	485935	9960.0	6471.6	7198.9	9645.0	4899.1	6200.1
GQ021761.1	487908	10221.1	5186.8	6302.2	9708.4	7158.5	7195.6
GQ045522.1	466285	11755.4	8347.2	14485.9	13082.8	8386.4	9513.9
GQ083081.1	414741	15877.5	12236.7	13991.0	14693.6	12163.8	11841.0
GQ023923.1	485746	15624.0	11085.5	12581.7	16345.7	9950.9	11623.1
GQ015141.1	494526	8385.3	4819.2	14843.7	12602.3	4314.3	6108.2

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GQ021661.1 gg_id:488008 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ047667.1 gg_id:388696 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137f03c1
GQ082922.1 gg_id:419241 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ023083.1 gg_id:486586 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ039204.1 gg_id:460327 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
GQ039224.1 gg_id:388202 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
GQ104344.1 gg_id:462415 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ060037.1 gg_id:391627 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ115923.1 gg_id:428199 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw603a10
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GQ023682.1 gg_id:485985 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ023920.1 gg_id:485750 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
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GQ067203.1 gg_id:460265 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ060147.1 gg_id:397004 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ032383.1 gg_id:450904 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542a09
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GQ007419.1 gg_id:502246 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ059948.1 gg_id:412346 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ060022.1 gg_id:484585 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ108233.1 gg_id:386381 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw604b09
GQ103575.1 gg_id:386707 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ072717.1 gg_id:429703 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw20
GQ104463.1 gg_id:431199 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ045872.1 gg_id:465397 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ065193.1 gg_id:382362 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw84a02
GQ089325.1 gg_id:437797 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ105762.1 gg_id:462767 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ047682.1 gg_id:410867 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h03c
GQ038761.1 gg_id:467014 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu522g04
GQ022130.1 gg_id:487538 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ039163.1 gg_id:441418 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
GQ008890.1 gg_id:500775 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ107085.1 gg_id:410343 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw544e0
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GQ023940.1 gg_id:485729 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu

GQ108411.1	385971	10639.2	6837.9	12848.1	10763.5	4653.1	6322.8
GQ021661.1	488008	8129.1	4492.4	9643.5	8186.1	4020.3	5789.2
GQ047667.1	388696	21298.6	17567.7	14577.1	17356.2	17179.3	16387.2
GQ082922.1	419241	9628.8	3617.2	9402.8	8637.3	3587.3	5886.1
GQ023083.1	486586	8573.8	4533.8	10980.9	10307.2	4928.2	6564.3
GQ039204.1	460327	15108.2	12332.9	8534.3	12722.3	13035.4	12328.4
GQ039224.1	388202	6769.6	3841.7	10634.1	7905.2	3792.4	5002.4
GQ104344.1	462415	14783.1	11776.3	15621.6	15078.6	13617.9	13857.3
GQ060037.1	391627	9247.5	5558.3	6662.1	9370.8	5232.1	5209.7
GQ096983.1	388915	10656.3	5692.8	10816.0	12768.4	6118.2	8158.2
GQ115923.1	428199	17166.2	12531.2	6812.0	16025.8	11752.3	11957.5
GQ009005.1	500661	15539.8	12764.7	17161.2	16391.5	11881.9	13073.7
GQ037083.1	447493	16196.0	12764.0	15269.3	16041.1	15608.4	14594.4
GQ021769.1	487899	10023.3	5721.3	11193.6	13712.6	7310.1	7697.6
GQ037353.1	434630	10876.8	7785.4	3506.9	13487.8	10350.3	10409.9
GQ023682.1	485985	17582.7	13616.0	16696.1	16567.6	12532.3	13365.3
GQ023920.1	485750	8706.5	6495.4	7065.3	7297.8	7217.9	8081.2
GQ060082.1	425951	14549.5	13984.1	10616.8	15307.9	15756.5	13281.3
GQ067203.1	460265	13803.9	13298.5	8914.4	16982.0	17375.4	14514.0
GQ060147.1	397004	12629.1	8084.5	9281.4	13148.5	10878.3	10759.7
GQ032383.1	450904	10396.0	4858.0	8113.7	13827.2	3975.6	5654.1
GQ113325.1	422526	6416.8	5695.3	5867.7	8048.2	4501.8	6018.8
GQ007419.1	502246	20675.6	17155.6	13142.6	18647.2	16227.7	15663.0
GQ059948.1	412346	14896.9	11407.3	16967.0	16572.5	13657.1	14804.4
GQ060022.1	484585	6693.4	2357.6	7292.5	6847.4	2022.2	4494.0
GQ108233.1	386381	7785.4	2316.1	6400.4	8079.8	2989.9	3897.4
GQ103575.1	386707	5737.6	2523.4	5028.6	7496.5	3404.3	3218.4
GQ072717.1	429703	8056.8	3750.1	10702.8	10075.7	2880.0	6064.5
GQ104463.1	431199	11452.2	6709.6	10685.7	10657.5	7618.7	8928.3
GQ045872.1	465397	10915.5	6807.0	5981.8	9965.4	5246.1	6491.7
GQ065193.1	382362	9321.1	4391.3	9250.7	9175.8	5449.6	6787.0
GQ089325.1	437797	13786.3	10127.7	6930.0	13958.9	14374.9	13663.1
GQ105762.1	462767	11576.3	11355.0	11204.8	12310.0	9394.5	11715.4
GQ047682.1	410867	15408.8	11903.8	15116.2	15778.5	10928.6	11579.2
GQ038761.1	467014	13225.4	7951.0	14045.4	15672.1	10330.5	11021.3
GQ022130.1	487538	14546.2	9218.2	10656.1	13698.8	7667.9	9125.5
GQ039163.1	441418	12035.5	7067.6	15118.5	13379.2	6049.8	7635.2
GQ008890.1	500775	9684.6	3667.3	7539.7	8551.5	2552.3	4160.8
GQ107085.1	410343	16747.2	11458.1	9007.9	15841.4	13526.1	11891.5
GQ024659.1	485011	10169.1	5525.4	13474.1	11647.5	4575.4	7206.0
GQ023940.1	485729	9938.4	4218.6	11784.7	10028.8	5584.0	7827.5

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GQ072878.1	405335	10940.2	5751.8	14287.0	12606.5	6708.9	8127.3
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GQ008557.1	501108	9134.4	6512.1	10206.5	10868.6	5115.2	7748.8
GQ008246.1	501419	10444.8	9105.6	7997.6	12781.9	6710.8	8922.7
GQ023765.1	485905	7811.8	4953.6	5986.0	7681.2	3713.4	4862.0
GQ070561.1	421989	14688.3	11084.0	7586.4	15786.7	12592.1	11150.7
GQ039132.1	403296	10759.6	7122.4	12150.5	13671.2	6622.5	8279.7
GQ059972.1	447338	6530.1	3352.2	7197.9	8101.7	3300.2	6350.6
GQ024547.1	485123	10913.2	4855.0	12936.1	13654.0	3845.1	6590.5
GQ039028.1	449178	11098.8	9250.1	11030.6	7358.0	10667.0	10369.7
GQ021079.1	488589	10972.0	4062.0	4598.7	13406.7	2242.1	4843.4
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GQ108828.1 gg_id:427596 Topographical and Temporal Human Skin Microbiome skin palm clone nbw718b02c1
GQ047944.1 gg_id:422929 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139d03c1
GQ023184.1 gg_id:486485 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2
GQ022504.1 gg_id:487165 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ102484.1 gg_id:438661 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ023735.1 gg_id:485938 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ007376.1 gg_id:502290 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ105971.1 gg_id:383810 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw.
GQ007629.1 gg_id:502036 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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GQ001502.1	508160	12741.4	6996.4	12028.2	12625.2	5644.6	7536.1
GQ038987.1	416468	15818.8	11445.0	12355.9	19577.0	12778.8	11954.2
GQ109039.1	405200	11429.2	9551.7	13504.4	13101.3	13188.7	11858.5
GQ039287.1	465090	10707.4	4135.4	9799.9	9620.9	3858.7	6166.1
GQ023583.1	486086	8027.6	5031.8	11038.5	9820.3	4104.5	6792.9
GQ103900.1	434514	7087.3	3555.4	10136.0	10801.4	2313.0	5663.4
GQ092143.1	383408	16405.3	12768.1	9718.3	18063.5	17587.4	16372.6
GQ070449.1	413775	20378.0	18477.7	17592.4	18114.2	16263.1	17246.3
GQ105745.1	375098	15366.7	11645.5	12416.8	15075.9	10728.6	12721.6
GQ093426.1	438452	7546.5	6213.6	9266.3	11464.1	8042.7	10208.7
GQ023216.1	486452	9913.8	3918.3	9338.5	9496.8	4424.5	6355.7
GQ103053.1	406427	10754.8	4402.0	12730.5	10978.4	3447.6	5293.6
GQ065894.1	383660	8785.7	3118.0	8052.4	8483.2	3058.0	5058.2
GQ091469.1	397168	10309.4	7064.9	7884.5	13106.9	10706.3	10057.7
GQ038900.1	389164	8852.7	4926.3	9091.9	9229.8	3184.9	5965.9
GQ008263.1	501402	12848.3	10074.9	13955.1	12579.2	7536.2	9517.8
GQ007168.1	502497	11792.1	6034.6	13831.8	13631.3	4890.2	8076.1
GQ105059.1	431480	9099.8	7649.5	11262.9	12677.8	11290.2	9687.5
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GQ103487.1	409642	17362.6	11324.4	12719.9	18679.6	9286.8	11792.2
GQ023503.1	486166	11664.0	5551.4	12131.7	12337.3	5145.0	7629.1
GQ039725.1	389917	6897.7	5016.5	6118.0	10126.8	7199.7	8732.0
GQ093392.1	377863	8056.7	3604.7	8306.5	7177.2	3203.1	5025.5
GQ090523.1	383565	19938.6	16238.3	13016.8	16798.7	14718.7	15469.2
GQ105155.1	383681	11565.9	10257.4	11897.9	14058.5	11636.8	10959.7
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GQ106355.1	415219	11863.7	10697.0	6154.0	14311.8	15584.8	13864.0
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GQ108828.1	427596	6826.8	5084.6	4824.0	6777.4	4025.1	4688.4
GQ047944.1	422929	10076.2	6528.6	6487.0	12076.9	4642.9	7683.6
GQ023184.1	486485	13709.3	9421.0	7577.9	15765.7	11725.5	11873.2
GQ022504.1	487165	10980.1	7833.6	11649.0	11589.0	9054.2	10050.6
GQ102484.1	438661	11452.6	6717.6	8529.1	12733.0	6870.9	9936.3
GQ023735.1	485938	7751.2	4473.1	7315.3	8166.8	4160.2	5289.6
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GQ105971.1	383810	7850.2	4853.7	11334.1	9336.5	3726.3	7146.4
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GQ114623.1 gg_id:382109 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ107070.1	438337	16681.9	12519.4	18455.5	18088.5	11568.3	12611.0
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GQ087493.1	451924	24951.3	21788.9	24561.9	19890.6	22256.5	20885.1
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GQ023654.1	486015	20946.8	16806.8	18559.0	20129.9	15463.3	16410.2
GQ008754.1	500911	15611.3	12577.2	9340.4	11961.6	12279.5	12037.8
GQ105222.1	376488	15452.8	13728.7	15260.9	15776.4	15090.8	13544.9
GQ008654.1	501008	10758.8	6931.0	13310.0	12550.7	5484.2	8450.9
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GQ103594.1	382195	7585.4	3226.3	8208.7	7047.7	4530.7	5932.2
GQ023276.1	486394	8597.9	3764.8	10259.5	9476.0	4826.8	6061.9
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GQ038728.1	381792	8683.6	5081.4	14320.5	11828.8	6961.7	7773.3
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GQ070559.1 gg_id:427955 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw2
GQ108430.1 gg_id:417610 Topographical and Temporal Human Skin Microbiome skin palm clone nbw606e09c1
GQ022061.1 gg_id:487608 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ021058.1 gg_id:488610 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2
GQ060126.1 gg_id:387918 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ096069.1 gg_id:418452 Topographical and Temporal Human Skin Microbiome skin back clone nbw386b10c1
GQ092668.1 gg_id:394657 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ007131.1 gg_id:502532 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ105312.1 gg_id:437116 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ060001.1 gg_id:430098 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ024368.1 gg_id:485302 Topographical and Temporal Human Skin Microbiome skin palm clone nbw121f07c1
GQ105841.1 gg_id:372071 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ007269.1 gg_id:502401 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ106017.1 gg_id:441683 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ096151.1 gg_id:455391 Topographical and Temporal Human Skin Microbiome skin back clone nbw387d04c1

GQ024475.1	485195	12865.2	10561.6	6755.1	13636.8	15166.9	13076.3
GQ114506.1	428619	9875.3	6962.0	7079.6	8049.8	6689.3	7280.5
GQ113259.1	440687	9516.4	4382.6	9651.2	9365.4	4433.6	6052.8
GQ024772.1	484898	9974.3	8300.5	9092.4	11331.8	7478.8	8205.3
GQ108753.1	428664	10077.2	4324.4	11304.2	10526.1	4857.4	6689.9
GQ023685.1	485986	3958.6	2217.9	4188.1	4963.2	2207.0	3329.4
GQ089304.1	385255	9610.9	4227.0	11260.3	11469.3	3174.1	6835.5
GQ115920.1	438462	8048.4	4059.2	4266.1	7721.5	2645.6	3999.6
GQ114224.1	425361	7781.3	7713.4	8925.9	10692.9	8272.0	8182.9
GQ038678.1	444551	9419.1	5823.2	12826.3	10806.7	4728.6	6443.3
GQ051317.1	390582	9500.3	4431.8	12478.6	10099.2	6139.9	7415.1
GQ105233.1	382024	6869.8	2987.5	6209.0	6343.9	2590.1	3530.3
GQ024336.1	485334	11534.2	8003.8	12157.5	12363.1	10279.1	11706.6
GQ023197.1	486472	9452.7	6228.3	13342.3	11854.2	4668.2	7862.4
GQ021966.1	487703	10446.9	7189.2	12706.8	13695.2	11392.8	10543.8
GQ023722.1	485948	18988.9	14152.5	26336.7	23831.1	16965.4	19754.1
GQ049054.1	433002	5694.0	3513.5	7201.8	13912.9	2454.0	6533.3
GQ109110.1	412922	7830.9	4792.8	10240.2	9709.5	3718.7	7195.3
GQ021443.1	488225	10424.1	9435.5	9025.6	10741.5	9300.4	9435.3
GQ073039.1	434889	11791.0	6082.2	14952.1	14005.1	4901.9	8109.8
GQ105807.1	459856	10357.1	3944.2	11077.0	11716.6	3200.1	5267.0
GQ008455.1	501209	6889.5	3119.4	10228.7	8946.3	4586.9	5366.0
GQ007295.1	502370	8374.1	5493.3	4648.7	13425.8	5469.3	8831.1
GQ025221.1	457365	10518.9	6381.0	7694.6	11347.5	7941.6	7498.0
GQ089194.1	426243	10450.0	3646.7	9472.7	9560.0	4056.8	6149.4
GQ102502.1	384320	11460.4	5343.7	12373.5	14150.8	4471.5	7523.5
GQ070559.1	427955	9564.4	5935.5	5604.7	8532.0	6329.9	7008.0
GQ108430.1	417610	7385.3	2662.2	7625.7	7349.1	3258.1	4889.5
GQ022061.1	487608	6915.0	5288.8	12250.5	9748.3	4278.6	6866.4
GQ021058.1	488610	17939.3	14097.9	13487.6	15107.3	14705.2	12791.6
GQ060126.1	387918	12630.2	8036.9	8161.1	12799.7	10865.8	10726.0
GQ096069.1	418452	12901.5	9647.5	15180.7	13862.1	9666.0	10734.5
GQ092668.1	394657	13356.3	9365.0	14119.2	15402.5	12040.0	10988.5
GQ007131.1	502532	11775.8	10412.5	7577.9	13779.6	14614.7	13191.2
GQ105312.1	437116	8333.3	3618.2	4670.4	8946.8	3447.3	5743.0
GQ060001.1	430098	10163.1	5941.2	14423.5	12249.3	6600.5	7369.3
GQ024368.1	485302	10938.7	4077.8	10489.1	9742.1	3855.2	6916.6
GQ105841.1	372071	14169.4	12639.7	13342.9	13281.5	12826.5	11357.7
GQ007269.1	502401	8166.0	4286.4	9070.1	8724.3	4463.5	6540.6
GQ106017.1	441683	7351.7	3029.8	10320.7	8805.2	2937.1	5042.0
GQ096151.1	455391	20331.3	18464.4	12128.8	16403.2	17651.8	17176.1

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GQ037819.1 gg_id:446629 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ007149.1 gg_id:502514 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ009026.1 gg_id:500640 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ025332.1 gg_id:429299 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ102360.1 gg_id:382685 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ102181.1 gg_id:454910 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ045526.1 gg_id:428645 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ023304.1 gg_id:486366 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2
GQ023667.1 gg_id:486002 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ095669.1 gg_id:382891 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ021664.1 gg_id:488004 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ023678.1 gg_id:485990 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ037473.1 gg_id:466984 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ087575.1 gg_id:456694 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ022807.1 gg_id:486862 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ059793.1 gg_id:408365 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ008229.1 gg_id:501436 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ108198.1 gg_id:463808 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw603f05c
GQ102872.1 gg_id:436829 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ114736.1 gg_id:445164 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ016965.1 gg_id:492702 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu114
GQ062968.1 gg_id:407010 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw96a05c
GQ108844.1 gg_id:432413 Topographical and Temporal Human Skin Microbiome skin palm clone nbw718c07c1
GQ073043.1 gg_id:379640 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204d09c
GQ105239.1 gg_id:372433 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ037180.1 gg_id:398671 Topographical and Temporal Human Skin Microbiome skin palm clone nbu389h03c1
GQ105289.1 gg_id:394627 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ064941.1 gg_id:457050 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw81b07
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GQ021635.1 gg_id:488033 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu28
GQ113083.1 gg_id:405705 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ114028.1 gg_id:380944 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ007174.1 gg_id:502490 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ033025.1 gg_id:392838 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ039267.1 gg_id:404773 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
GQ038068.1 gg_id:414649 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu37
GQ060030.1 gg_id:454701 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

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GQ037819.1	446629	9793.3	4297.3	11311.9	11488.3	3198.9	6954.2
GQ007149.1	502514	8743.5	4788.9	13288.6	11524.6	3757.0	6611.6
GQ009026.1	500640	6859.3	3247.7	6376.2	7748.5	2994.5	5877.6
GQ025332.1	429299	9050.8	5875.7	8547.4	10081.9	7456.0	7533.7
GQ102360.1	382685	16114.3	11731.0	15099.2	16646.9	13174.2	14070.2
GQ102181.1	454910	9537.6	3170.4	8812.6	10405.5	2964.0	4789.9
GQ045526.1	428645	9588.3	4980.7	9826.6	9854.9	6313.1	7723.6
GQ023304.1	486366	10265.2	6009.6	12079.6	11295.6	4695.7	7100.9
GQ023667.1	486002	7706.2	2511.9	8980.6	9410.6	2656.4	5097.5
GQ095669.1	382891	9996.1	4557.3	12076.7	11465.1	3582.9	6538.1
GQ021664.1	488004	16481.7	13030.8	12652.0	13056.0	9720.1	9920.4
GQ023678.1	485990	10373.1	5980.8	11203.5	11260.1	4690.2	7159.3
GQ037473.1	466984	11774.2	9630.7	6774.6	15108.5	11236.2	10652.8
GQ087575.1	456694	14317.5	7654.8	9328.0	14701.9	8428.0	8153.3
GQ022807.1	486862	14906.7	12016.3	17377.1	15607.0	14452.0	14391.7
GQ059793.1	408365	14480.0	9621.9	13075.8	13135.3	8321.9	10004.6
GQ104856.1	386292	3464.2	1637.9	6255.7	4716.4	2083.4	4507.0
GQ115301.1	418560	10430.8	4352.0	13952.2	10130.5	2492.2	6758.2
GQ008025.1	501640	11061.2	6992.8	11190.1	11495.7	5138.6	7701.8
GQ008229.1	501436	8745.9	6596.6	6254.8	6845.1	7309.4	8160.7
GQ108198.1	463808	7554.3	5293.9	5783.9	9195.1	6917.9	7376.7
GQ102872.1	436829	7706.2	2511.9	8980.6	9410.6	2656.4	5097.5
GQ114736.1	445164	9914.4	4032.2	8520.6	8659.5	3557.6	6019.3
GQ016965.1	492702	13612.5	10948.8	10594.7	16062.2	16196.0	15330.6
GQ062968.1	407010	9327.2	2823.5	7822.0	8245.4	2575.3	5122.9
GQ108844.1	432413	9800.3	3669.3	10419.4	9070.3	3827.4	6122.6
GQ073043.1	379640	4518.7	1973.5	5689.8	5462.3	1829.4	3373.0
GQ105239.1	372433	17924.4	14426.3	12119.6	17133.3	10846.9	13050.9
GQ037180.1	398671	3771.0	3818.0	15691.4	10916.1	3176.1	5490.5
GQ105289.1	394627	13908.7	8968.2	11006.2	15446.1	9235.2	10985.5
GQ064941.1	457050	10313.6	4586.0	9785.7	11513.9	4374.3	6917.6
GQ106744.1	375176	12773.1	8546.7	7651.2	14710.0	12422.4	12650.4
GQ021635.1	488033	9859.8	5145.4	8598.7	9323.6	5065.7	7466.7
GQ113083.1	405705	7800.0	2469.7	7099.0	9167.5	1560.1	4565.5
GQ114028.1	380944	13251.8	12761.4	7141.6	13971.4	14647.8	12896.9
GQ007174.1	502490	7925.8	2420.3	9017.7	7217.7	2650.7	4178.8
GQ033025.1	392838	8036.9	4681.1	10331.6	9238.6	5163.7	7061.5
GQ039267.1	404773	8167.5	5403.3	5394.5	10319.3	8987.1	9746.9
GQ038068.1	414649	9318.7	6449.8	10614.6	10179.6	4821.5	6825.8
GQ060030.1	454701	11998.5	8142.4	9193.6	13618.6	9607.7	9246.6

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AB076855.1 gg_id:30289 Diaphorobacter nitroreducens str. KSP3
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GQ007509.1	502156	8193.4	3497.8	7607.4	7741.0	4190.9	6037.6
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GQ033045.1	390589	10937.0	6871.8	12094.2	10743.0	5027.4	6939.5
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GQ074865.1	439805	9881.4	4634.7	8103.6	11166.1	6977.1	8416.9
GQ018292.1	491376	8850.1	5165.3	9341.3	8112.7	4337.5	6565.5
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GQ108422.1	404678	9600.2	3729.0	9302.8	9407.7	3877.3	6062.7
GQ108405.1	388964	8070.3	4339.4	6566.6	9239.1	4745.3	7707.7
GQ038970.1	404635	17288.3	12328.0	15748.4	16181.1	11715.2	11775.5
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GQ023018.1	486651	8297.2	3110.1	8393.1	9906.4	2688.7	5100.5
GQ106663.1	459845	14756.0	11757.8	15683.2	14874.4	14162.8	14151.4
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GQ085368.1 gg_id:468029 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw274f03c
GQ038990.1 gg_id:461469 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ075411.1 gg_id:452993 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ108887.1 gg_id:415271 Topographical and Temporal Human Skin Microbiome skin palm clone nbw718g10c1
GQ105738.1 gg_id:416564 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ008355.1 gg_id:501310 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ032927.1 gg_id:376081 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ020733.1 gg_id:488935 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ113339.1 gg_id:451331 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ089012.1 gg_id:373372 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ021034.1 gg_id:488634 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2
GQ104173.1 gg_id:430167 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw564d0
GQ098625.1 gg_id:448016 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw704e
GQ024492.1 gg_id:485178 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123a02c1
GQ008416.1 gg_id:501249 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ007127.1 gg_id:502538 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ105852.1 gg_id:396103 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ062269.1 gg_id:453689 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ008098.1 gg_id:501567 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ024335.1 gg_id:485335 Topographical and Temporal Human Skin Microbiome skin palm clone nbw121c08c1
GQ037560.1 gg_id:437662 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ092641.1 gg_id:441412 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc

GQ110999.1	371123	16063.6	13180.8	13052.4	17642.1	12434.5	13248.4
GQ038073.1	400846	8658.0	4173.7	10332.7	8847.3	3946.0	6649.0
GQ008519.1	501146	14949.4	14618.9	13376.7	15739.3	15769.5	14217.5
GQ088096.1	411931	5222.6	3234.6	4385.0	6273.8	3996.7	4278.8
GQ023651.1	486018	10705.3	5971.3	12130.4	11794.6	4494.2	7788.9
GQ008687.1	500978	11323.6	4925.0	13046.4	11560.2	4804.2	7514.6
GQ101638.1	402732	12813.1	13312.3	14378.0	11756.8	14762.2	13918.1
GQ007150.1	502516	9756.8	5038.5	5869.3	10109.9	7371.2	7051.3
GQ116239.1	373028	17819.2	14974.7	17669.5	19038.7	18719.8	17837.7
GQ108798.1	446567	12580.0	4063.5	10645.3	10050.8	4577.7	6651.2
GQ023211.1	486460	12074.8	5296.6	10147.2	12137.0	3574.0	6576.9
GQ113082.1	438655	10409.1	8670.0	12970.2	12798.1	15299.7	12117.6
GQ098218.1	416329	9163.5	3365.2	10723.4	10714.7	1987.4	4375.1
GQ070693.1	382844	7459.4	2836.5	8438.2	7879.7	3042.3	4158.2
GQ047676.1	379460	13549.1	10162.6	10519.7	10480.1	8918.7	9249.4
GQ008935.1	500730	8807.3	3100.2	10620.3	8551.0	3195.5	5411.2
GQ106923.1	462030	13143.1	10256.6	9173.5	15794.0	10299.0	10578.8
GQ113776.1	373180	7567.5	3026.9	7378.0	8809.8	2697.0	4957.2
GQ103801.1	400569	13740.2	10152.8	8169.9	11932.5	9775.1	9908.3
GQ085368.1	468029	5937.4	3064.0	6075.3	7302.7	2399.4	4682.6
GQ038990.1	461469	11305.3	9165.5	13270.8	12717.3	9494.1	10124.4
GQ075411.1	452993	7706.2	2511.9	8980.6	9410.6	2295.9	5097.5
GQ108887.1	415271	20616.2	17184.1	10621.3	17394.0	17484.4	15545.7
GQ105738.1	416564	7808.8	4570.5	12206.1	11000.0	3242.0	6879.0
GQ008355.1	501310	3620.1	1781.1	4113.8	3846.7	1705.9	2433.7
GQ032927.1	376081	6525.4	2350.8	5305.4	6724.2	3294.0	4950.8
GQ020733.1	488935	12900.7	10956.5	9946.5	13828.1	9493.8	10658.9
GQ113339.1	451331	10608.6	6577.6	8506.7	10467.8	4740.8	6480.0
GQ089012.1	373372	13016.7	6783.0	13724.0	13989.9	8929.6	9525.1
GQ021034.1	488634	7928.7	3239.6	6526.2	7807.8	1781.4	3830.3
GQ104173.1	430167	11812.4	7076.2	12549.7	11869.8	7405.2	9010.3
GQ098625.1	448016	12731.8	7848.6	13455.8	13280.2	9392.6	9663.3
GQ024492.1	485178	10333.1	7135.1	10715.3	10779.3	7415.9	9271.8
GQ008416.1	501249	11403.7	10325.6	10179.8	12200.7	13170.8	11153.1
GQ007127.1	502538	3073.5	744.4	1218.6	2414.2	716.8	1346.6
GQ105852.1	396103	12180.4	8118.9	8391.4	13793.8	11092.7	11501.4
GQ062269.1	453689	10154.9	4445.2	10716.4	12789.8	2903.5	7174.5
GQ008098.1	501567	9889.5	3481.6	9576.8	9953.6	1890.0	5219.8
GQ024335.1	485335	8863.0	4390.0	9695.9	8757.6	4928.4	6186.8
GQ037560.1	437662	15978.7	11440.4	9434.8	15510.2	12160.4	11992.4
GQ092641.1	441412	11114.4	7657.2	7349.3	9357.3	8140.4	9334.6

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GQ114104.1 gg_id:462948 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ112319.1 gg_id:413318 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ091995.1 gg_id:387528 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ102140.1 gg_id:400863 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561e1
GQ038056.1 gg_id:376214 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu37
GQ024328.1 gg_id:485343 Topographical and Temporal Human Skin Microbiome skin palm clone nbw121c01c1
GQ023567.1 gg_id:486102 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320b05
GQ101851.1 gg_id:439257 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw500a09c
GQ115371.1 gg_id:383152 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ105415.1 gg_id:422303 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ007221.1 gg_id:502441 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ111534.1 gg_id:441719 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw581
GQ113712.1 gg_id:407160 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ107439.1 gg_id:430760 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ100730.1 gg_id:463219 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ060035.1 gg_id:420537 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ045508.1 gg_id:453490 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ102400.1 gg_id:465182 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
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GQ008522.1 gg_id:501144 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ037915.1 gg_id:388673 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ023642.1 gg_id:486026 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ045856.1 gg_id:450910 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ024378.1 gg_id:485294 Topographical and Temporal Human Skin Microbiome skin palm clone nbw121g06c1
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GQ023469.1 gg_id:486201 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319a09
GQ000354.1 gg_id:468919 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
GQ052705.1 gg_id:435714 Topographical and Temporal Human Skin Microbiome skin back clone nbu539h03c1
GQ023024.1 gg_id:486645 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ023122.1 gg_id:486547 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu3(
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GQ096531.1 gg_id:416850 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw389d0

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GQ114104.1	462948	10208.2	4787.6	10373.2	12698.3	4871.3	7481.4
GQ112319.1	413318	10075.9	4663.9	9153.2	9201.9	4816.2	6567.2
GQ091995.1	387528	11544.7	6115.7	10382.4	13508.8	5119.7	6661.6
GQ102140.1	400863	8806.5	3307.9	8761.2	8176.1	3043.5	4983.9
GQ038056.1	376214	11679.3	7932.6	13538.9	13464.6	9031.1	9986.3
GQ024328.1	485343	6931.0	3860.0	10618.8	9571.5	3789.3	6031.8
GQ023567.1	486102	12904.1	5932.6	14623.6	10865.9	5146.8	7826.3
GQ101851.1	439257	16439.2	10003.1	18695.4	16094.1	6637.0	8728.5
GQ115371.1	383152	13948.7	11099.8	8744.4	9761.3	13016.6	12106.7
GQ105415.1	422303	12105.8	8949.9	6442.4	14601.3	13795.7	13265.7
GQ007221.1	502441	11371.8	9521.1	12659.7	13207.5	12053.2	13972.5
GQ111534.1	441719	16912.5	11903.4	10834.4	18702.9	12505.7	11325.1
GQ113712.1	407160	9801.6	6312.1	14759.5	13002.5	4657.2	8014.6
GQ107439.1	430760	8578.3	2868.8	9455.1	10578.0	2622.7	5179.4
GQ100730.1	463219	10386.2	6228.8	14957.7	10995.8	4207.0	7689.6
GQ060035.1	420537	9139.2	2747.5	8425.9	7981.6	2802.9	4824.8
GQ045508.1	453490	19105.4	17059.8	10589.3	13891.8	16155.5	15221.0
GQ102400.1	465182	9332.7	4456.6	10349.3	8838.4	5457.7	6734.9
GQ023957.1	485712	9675.2	4172.1	12182.5	10679.3	3085.9	6178.1
GQ008522.1	501144	8217.5	3702.1	7887.7	8143.6	2259.4	4234.3
GQ037915.1	388673	6818.2	3290.5	7954.1	8557.6	4034.8	6034.3
GQ101891.1	442572	1289.8	894.9	3486.5	2601.2	705.0	950.6
GQ023642.1	486026	7987.9	4770.7	5159.0	9382.0	4193.1	6541.0
GQ045856.1	450910	16583.3	10643.7	17538.2	17218.3	11332.9	13247.5
GQ024378.1	485294	7520.9	7220.9	8148.8	9935.7	7555.6	8075.8
GQ037288.1	383487	11167.5	7372.8	11296.1	10417.5	5620.8	7415.4
GQ023469.1	486201	13150.7	7107.5	17411.3	16014.4	6957.2	9369.8
GQ000354.1	468919	16042.1	12606.7	6905.2	11836.5	13182.7	12592.7
GQ052705.1	435714	10398.4	4073.9	8904.4	9911.9	4340.5	6395.0
GQ023024.1	486645	14656.0	12443.4	11433.1	16026.9	13812.3	12822.1
GQ023122.1	486547	8244.6	3638.7	9012.6	8750.6	3089.9	5753.6
GQ037251.1	448906	9149.1	4446.9	10421.7	8631.2	4898.5	6762.1
GQ025066.1	446103	8527.0	3992.7	6220.2	8102.3	3365.8	5315.0
GQ104239.1	414271	8487.6	7232.3	5035.6	11238.6	12855.2	12098.3
GQ008425.1	501240	10450.1	5427.6	9695.8	9433.2	5661.5	6863.3
GQ091549.1	457989	5574.1	3261.3	3850.7	6853.8	4157.0	4541.8
GQ097206.1	451738	14712.1	10008.2	14215.8	13247.2	9738.2	11304.7
GQ115410.1	427119	7460.0	4486.7	10788.9	9708.7	2975.3	6726.8
GQ022859.1	486810	21557.7	19860.4	20466.8	18165.2	21062.5	19175.7
GQ096531.1	416850	8887.0	4539.7	9667.9	9599.7	5052.7	6941.6

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GQ105786.1	461385	17199.7	15458.2	7089.8	15374.9	13568.0	13097.1
GQ104677.1	408146	9894.9	6080.9	9381.8	9523.2	5685.9	6414.3
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GQ022266.1	487406	8935.4	4414.6	8374.0	9130.5	5540.8	7009.7
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GQ007283.1	502381	12073.6	6501.8	11360.5	12390.9	9242.2	10326.5
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GQ092690.1	461460	15967.3	10363.5	13196.2	19182.8	10761.6	11074.6
GQ096095.1	452340	8135.1	6194.0	5269.4	13426.2	4654.2	8556.7
GQ114786.1	390805	8492.4	3257.6	12489.1	8704.4	3168.2	4948.9
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GQ105065.1	427602	9295.3	3149.6	9698.6	9001.3	2497.9	4887.1
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GQ113125.1	381252	17173.8	11796.2	9460.5	12914.6	14032.3	13386.9
GQ048213.1	444064	11810.7	9463.4	11820.4	12223.3	10460.1	10714.5
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GQ092699.1 gg_id:396262 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl

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GQ024446.1	485224	13483.9	9857.4	7891.7	14662.1	13788.4	10105.6
GQ096989.1	433677	9621.7	4209.0	11462.0	10682.4	5138.4	5660.5
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GQ107194.1	378320	18866.8	16695.8	15568.1	17101.5	16507.6	15633.8
GQ025032.1	449110	15296.6	10331.3	15634.8	18478.3	9845.9	12149.3
GQ075548.1	384590	15089.4	10966.5	16544.1	16967.2	12703.8	14230.8
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GQ112866.1	425565	14474.3	9815.2	6985.5	15630.7	11740.4	12030.3
GQ024991.1	484679	8979.3	6076.6	7120.5	8710.8	4872.3	6042.2
GQ007474.1	502190	14963.7	13216.4	9858.4	11325.3	13851.3	12684.7
GQ114078.1	411458	15067.5	11180.3	9202.2	11804.0	10255.6	10396.0
GQ093400.1	411484	14753.3	11944.0	8120.7	17504.3	17317.2	13942.6
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GQ023357.1	486312	8332.5	3473.3	8055.9	9600.5	4039.1	5912.7
GQ095852.1	395840	9278.5	5306.2	8746.7	7777.6	4908.1	5488.6

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GQ023229.1	486440	8516.5	10371.3	7980.6	8953.8	9900.5	9393.9
GQ104447.1	435787	9505.5	3571.0	8903.1	8558.0	3408.0	5752.7
GQ022371.1	487298	6421.8	3054.4	8648.3	8595.7	2269.8	5721.2
GQ023269.1	486402	13595.1	9349.6	5246.3	16057.7	13062.7	12287.8
GQ095726.1	393055	8344.2	3511.0	10354.1	9933.7	2686.0	5188.7
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GQ102415.1	384324	9992.4	7714.6	7833.2	11808.3	11194.5	10429.0
GQ008410.1	501256	20571.1	17006.0	14097.6	16803.1	16611.4	15347.2
GQ060113.1	436416	7255.5	5311.2	5523.3	8685.0	4521.4	6719.9
GQ092679.1	445801	10197.1	5169.0	13271.1	11255.4	7748.5	8606.6
GQ047931.1	390789	10672.2	5746.5	9236.7	10868.0	6656.0	7095.7
GQ007279.1	502384	12852.0	12277.6	18792.3	13498.8	9385.7	9724.3
GQ096479.1	395307	9885.6	8005.6	10370.8	12338.8	9901.8	10560.6
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GQ023775.1	485894	20700.1	21078.8	17575.9	19517.0	16565.2	16786.4
GQ023499.1	486170	9799.4	4293.0	11278.4	11485.9	3197.2	6940.5
GQ060107.1	451805	12134.6	9039.9	12247.8	11105.8	9317.0	10300.6
GQ038630.1	393127	9358.8	4738.9	10316.3	9285.8	5934.3	7577.7
GQ105776.1	419815	8081.1	5991.5	12218.1	10444.9	5094.5	7454.9
GQ102477.1	431344	10186.2	4506.8	12297.2	10724.7	5340.3	6494.2
GQ045821.1	455832	7731.0	4702.9	5453.9	9032.1	2275.2	3481.1
GQ023320.1	486348	12209.2	7512.9	10044.6	10809.9	8843.6	9265.4
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GQ008607.1	501058	9570.9	5182.2	6122.6	10013.6	4603.9	7465.4
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GQ069205.1	375233	9312.5	5041.1	8077.3	9103.8	7667.8	8196.5

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GQ007523.1 gg_id:502141 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ059901.1 gg_id:388118 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ039126.1 gg_id:428883 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
GQ021986.1 gg_id:487683 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ071439.1 gg_id:451605 Topographical and Temporal Human Skin Microbiome skin back clone nbw240b07c1
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GQ092105.1 gg_id:423190 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw406b05c
GQ098137.1 gg_id:463018 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ023700.1 gg_id:485973 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ087848.1 gg_id:405792 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359e0
GQ047623.1 gg_id:446578 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137a01c1
GQ008724.1 gg_id:500946 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ075357.1 gg_id:428756 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ007311.1 gg_id:502354 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ102281.1 gg_id:394061 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ096583.1 gg_id:449296 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw390a0
GQ105901.1 gg_id:374543 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ023168.1 gg_id:486500 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu3(
GQ086431.1 gg_id:414825 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw28
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GQ103750.1 gg_id:447744 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw700h02
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GQ023773.1 gg_id:485897 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ106270.1 gg_id:395529 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ022240.1 gg_id:487429 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ102202.1 gg_id:411312 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ023892.1 gg_id:485777 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu

GQ021674.1	487994	11652.6	6912.3	8963.2	12484.4	6360.5	8686.4
GQ065139.1	415822	8800.2	4004.0	11501.0	9330.4	4775.6	6981.5
GQ041447.1	434217	13363.2	8787.0	10517.0	14239.1	9958.2	9769.4
GQ045820.1	377023	15076.0	10953.2	16570.5	18166.2	12708.0	14313.4
GQ022181.1	487487	9109.7	3162.0	8419.2	7762.6	2826.9	4792.7
GQ102369.1	419878	5901.9	5614.6	5221.2	8709.9	10723.4	9178.0
GQ007523.1	502141	9798.2	4340.6	12398.7	11859.7	3208.9	6974.2
GQ059901.1	388118	15762.5	11181.2	13780.8	14425.4	10868.0	10818.6
GQ010590.1	499076	10711.3	5980.7	12247.3	11807.4	4494.7	7805.6
GQ039126.1	428883	23196.4	21185.1	22892.6	19626.2	21931.8	20057.9
GQ021986.1	487683	13466.7	6321.7	12292.6	12241.9	7299.6	7643.4
GQ071439.1	451605	8948.2	8720.8	8362.4	10263.7	9408.4	9536.0
GQ100754.1	424830	9864.2	3641.4	12445.5	12490.1	3655.4	6824.4
GQ047543.1	421363	8506.3	3392.2	8498.4	9596.1	2073.2	4328.2
GQ092105.1	423190	10168.8	3411.0	9855.9	11764.9	1439.1	3531.2
GQ098137.1	463018	9754.8	3870.5	10326.9	9668.0	3567.0	5743.9
GQ023700.1	485973	10387.1	4021.4	11179.9	9696.6	4530.2	6499.5
GQ087848.1	405792	7043.1	5464.4	7712.6	10275.6	8793.4	7906.0
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GQ008724.1	500946	9571.5	6847.5	14485.8	12938.9	9038.0	11536.8
GQ075357.1	428756	11483.6	9532.7	7928.7	9907.1	9531.4	9947.0
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GQ102281.1	394061	9412.7	4105.1	9152.3	8646.4	4509.6	5912.0
GQ096583.1	449296	11425.5	11360.5	10442.3	10372.4	13864.1	12409.2
GQ105901.1	374543	14057.2	10390.9	7436.7	14573.2	13072.0	10944.4
GQ023168.1	486500	7089.4	3104.4	4539.1	6911.8	2751.2	3841.9
GQ086431.1	414825	10692.8	6569.9	15765.8	14584.4	5599.5	8531.9
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GQ008542.1	501123	7903.5	3717.3	9609.3	8678.8	4151.5	5858.1
GQ007037.1	502624	14513.0	11265.9	15832.3	14989.2	10918.7	11187.1
GQ103750.1	447744	10618.6	4355.0	8815.7	8861.3	4192.0	6031.2
GQ045837.1	468105	6818.2	3290.5	7954.1	8557.6	4034.8	6034.3
GQ103968.1	432933	12358.6	7957.0	17537.6	14006.6	5904.1	8907.8
GQ062895.1	416524	8793.1	7036.0	13825.9	12464.7	6343.6	8908.3
GQ020735.1	488933	8874.9	5222.4	14205.1	13240.6	6601.6	7555.2
GQ105408.1	372301	17390.3	12904.4	15277.1	17071.2	9862.3	12311.0
GQ023773.1	485897	9486.6	5626.9	8180.1	11280.3	5072.7	6029.1
GQ106270.1	395529	9798.3	3510.1	8599.7	8671.8	3711.3	5865.5
GQ022240.1	487429	7842.5	3014.1	7449.2	10137.9	3254.6	4975.1
GQ102202.1	411312	9576.0	5350.8	9001.4	11707.2	5928.4	8227.9
GQ023892.1	485777	10809.2	6952.0	6365.2	9687.8	4673.1	7497.1

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GQ023914.1 gg_id:485755 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ075480.1 gg_id:427937 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ008061.1 gg_id:501604 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ083141.1 gg_id:425287 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ099937.1 gg_id:414923 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw475
GQ060118.1 gg_id:411821 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ060018.1 gg_id:393161 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ021439.1 gg_id:488229 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27
GQ110727.1 gg_id:388799 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ095410.1 gg_id:467596 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ102541.1 gg_id:396549 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
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GQ102392.1 gg_id:417667 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ103765.1 gg_id:375244 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ070640.1 gg_id:460073 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ105302.1 gg_id:375114 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
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GQ113850.1 gg_id:425541 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ008407.1 gg_id:501258 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ024065.1 gg_id:485603 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ015243.1 gg_id:494423 Topographical and Temporal Human Skin Microbiome skin palm clone nbw766b06c
GQ047997.1 gg_id:420323 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a10c1
GQ101864.1 gg_id:445697 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw500c01c
GQ033003.1 gg_id:384223 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ102838.1 gg_id:371553 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ089262.1 gg_id:413378 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw

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GQ008061.1	501604	11603.9	7760.9	8837.5	12558.3	8710.5	9546.3
GQ083141.1	425287	8525.7	5629.0	6037.3	8271.7	4778.0	6193.8
GQ099937.1	414923	12994.0	10866.9	10463.7	12008.1	11812.4	10786.6
GQ060118.1	411821	12033.9	8565.4	5227.3	14065.3	12867.3	13179.2
GQ060018.1	393161	17420.7	12932.1	12558.7	17139.0	13890.7	13550.3
GQ021439.1	488229	21462.3	18581.3	16907.7	20167.6	21186.6	18812.5
GQ110727.1	388799	13820.3	13899.8	8461.9	11011.6	13401.7	12326.2
GQ108301.1	451885	10757.7	6978.6	14430.4	12924.5	5495.9	8484.6
GQ115910.1	458736	9498.2	4445.4	10122.9	9343.0	6292.3	7256.3
GQ101866.1	409806	9565.6	4055.7	8663.8	8131.9	3082.0	4412.6
GQ003202.1	506462	22628.0	17516.3	19455.7	21033.3	19346.8	18798.5
GQ001592.1	508070	24560.2	19697.3	22779.2	21797.6	23926.6	21271.4
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GQ021838.1	487830	13726.4	10170.4	8220.9	10914.4	9806.9	10066.2
GQ069816.1	465243	9439.8	6110.9	8662.5	9888.6	5236.4	7230.7
GQ094470.1	425183	9781.5	3886.1	10703.3	9731.3	3868.9	5960.9
GQ111545.1	410486	6986.3	3507.7	2157.0	8217.2	2617.0	4007.3
GQ022003.1	487665	11566.9	7450.5	7638.0	12627.2	8801.7	7216.7
GQ060123.1	402957	7706.2	2511.9	8980.6	9410.6	2656.4	5097.5
GQ039559.1	399581	12589.2	12975.2	9634.9	11588.9	4560.6	6498.7
GQ095410.1	467596	13762.8	9092.1	9691.9	15235.8	11247.9	10952.5
GQ102541.1	396549	21769.2	17936.7	15015.8	18754.6	18714.2	16820.8
GQ070845.1	401466	15525.4	9029.8	16252.9	14594.1	11687.9	11280.2
GQ022669.1	487000	6979.9	3243.7	9572.5	8263.4	2571.4	4759.8
GQ102392.1	417667	5533.6	2667.1	12485.6	9474.7	2509.6	4320.0
GQ103765.1	375244	8741.6	6256.6	6044.4	7750.6	6504.5	7218.5
GQ070640.1	460073	7789.5	4510.4	11193.2	11475.7	3235.4	6931.3
GQ105302.1	375114	10149.8	5462.9	12380.2	12185.7	4567.8	7254.8
GQ024305.1	485368	7121.6	3353.5	10186.5	9380.0	2807.5	5944.4
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GQ047997.1	420323	7710.2	5685.4	12766.8	10444.0	4351.1	6986.4
GQ101864.1	445697	11871.7	7260.4	12508.7	11282.7	8890.5	10026.5
GQ033003.1	384223	8204.6	4415.2	10025.4	14291.7	4630.1	9321.4
GQ102838.1	371553	16588.0	15270.6	11172.5	14168.7	8293.5	9287.1
GQ089262.1	413378	8045.0	2823.1	10085.4	7921.6	3720.7	4925.3

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GQ113967.1 gg_id:431063 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ045556.1 gg_id:384605 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ032370.1 gg_id:388304 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu541g08
GQ038742.1 gg_id:451746 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu522d04
GQ104656.1 gg_id:407711 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
AB064317.1 gg_id:17812 Diaphorobacter nitroreducens str. NA10B
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GQ103663.1 gg_id:406540 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ025155.1 gg_id:404810 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw11
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AY780907.1 gg_id:142675 Giesbergeria kuznetsovii str. 412
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FM204951.1 gg_id:542160 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
EU130955.1 gg_id:236660 Hydrogenophaga sp. BAC57
NR_028716.1 gg_id:584669 Hydrogenophaga taeniospiralis str. 2K1; ATCC 49743
DQ861288.1 gg_id:167427 Hylemonella gracilis ZL
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FM178810.1 gg_id:307150 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu
EF063629.1 gg_id:176635 Microbial ecology autotrophic anaerobic denitrifying UASB reactor clone R1Cb86
EU882843.1 gg_id:338208 Ottowia sp. str. RB1-10B
AY081982.1 gg_id:68619 atrazine-catabolizing microbial presence methanol clone KRA30+15
EU464751.1 gg_id:300229 Hartmann's mountain zebra feces clone AFZEB_aaj70b10
CU927648.1 gg_id:564787 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ167470.1 gg_id:324457 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
CU919583.1 gg_id:541370 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GU455142.1 gg_id:530933 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir

GQ099485.1	400551	5324.5	1522.8	5292.9	4623.2	2211.5	3435.7
GQ024386.1	485284	25965.9	23354.7	23699.9	19870.4	22491.3	21185.3
GQ106590.1	400290	8994.0	3601.5	11772.3	10250.8	3259.4	5863.3
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GQ113967.1	431063	15322.8	13899.2	16576.6	18013.4	16963.2	16452.5
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GQ038742.1	451746	11756.5	10351.6	6484.0	14424.0	14607.1	13240.1
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AM922191.1	249731	3921.5	2809.6	3738.9	5436.8	2475.8	5307.6
AB269772.1	209980	6058.6	3117.1	7253.3	7966.6	4644.5	7005.5
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FM204951.1	542160	6429.9	3150.5	9340.1	11476.7	1319.2	5304.6
EU130955.1	236660	6526.7	3247.5	10562.7	9141.4	2942.3	5580.0
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s__Pelomonas aquatica	11895

CU920132.1 gg_id:567828 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU926935.1 gg_id:543300 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY512827.1 gg_id:106787 Acidovorax avenae str. S19n
AY379977.1 gg_id:97627 Acidovorax sp. str. AHL 5
FM178827.1 gg_id:332615 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu
CU920294.1 gg_id:542956 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
NR_029001.1 gg_id:568325 Ottowia thiooxydans str. K11; DSM 14619
AY291121.1 gg_id:99960 Lampropedia hyalina str. ATCC 43383
DQ054782.1 gg_id:137154 dog bite wound on cheek 2 year old boy
EU801615.1 gg_id:348067 It's all ranking aquatic Chesapeake Bay MD clone 3C002955
EU801564.1 gg_id:356256 It's all ranking aquatic Chesapeake Bay MD clone 3C002888
EU800320.1 gg_id:305174 It's all ranking aquatic Delaware Bay NJ clone 2C228369
EU800970.1 gg_id:335155 It's all ranking aquatic Delaware Bay NJ clone 2C229239
EU800733.1 gg_id:321700 It's all ranking aquatic Delaware Bay NJ clone 2C228912
AY662014.1 gg_id:137421 uranium-contaminated groundwater clone 300I-B10
EU800384.1 gg_id:305775 It's all ranking aquatic Delaware Bay NJ clone 2C228462
DQ234121.2 gg_id:143875 determined library mangrove clone DS037
EF121352.1 gg_id:206051 microbiota uninfected and Rickettsia-infected colonized cat fleas Ctenocephalides fel
EU800631.1 gg_id:346376 It's all ranking aquatic Delaware Bay NJ clone 2C228791
EU801033.1 gg_id:330659 It's all ranking aquatic Delaware Bay NJ clone 2C229327
FN428768.1 gg_id:535518 Looking India metagenomic approach Mahananda river water clone MRM1022
AM849433.1 gg_id:236107 Seasonality Piburger See clone PIB-22
EU801768.1 gg_id:314723 It's all ranking aquatic Chesapeake Bay MD clone 3C003139
EU801726.1 gg_id:332065 It's all ranking aquatic Chesapeake Bay MD clone 3C003089
FJ612396.1 gg_id:582407 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.1
FN428758.1 gg_id:567530 Looking India metagenomic approach Mahananda river water clone MRA2012
EU801561.1 gg_id:332569 It's all ranking aquatic Chesapeake Bay MD clone 3C002885
EU800965.1 gg_id:328912 It's all ranking aquatic Delaware Bay NJ clone 2C229230
AY947947.1 gg_id:141740 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
AY792257.1 gg_id:124653 Humic Lake clone CrystalBog021H12
DQ501305.1 gg_id:195239 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw
EU801645.1 gg_id:341378 It's all ranking aquatic Chesapeake Bay MD clone 3C002991
AY948061.1 gg_id:141397 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl
EU800346.1 gg_id:310935 It's all ranking aquatic Delaware Bay NJ clone 2C228402
FJ612165.1 gg_id:512885 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.4.43
AM849435.1 gg_id:243487 Seasonality Piburger See clone PIB-24
EF667919.1 gg_id:250266 Long-term maintenance species-specific microbiota basal metazoan Hydra epitheliun
EF667927.1 gg_id:245084 Long-term maintenance species-specific microbiota basal metazoan Hydra epitheliun
FJ612313.1 gg_id:533183 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.1.5
AY863096.1 gg_id:112283 wastewater treatment pool clone SXAU059
AM501437.1 gg_id:240464 Pelomonas aquatica str. CCUG52631

CU920132.1	567828	9125.4	3073.6	8637.9	10727.5	2035.1	3527.8
CU926935.1	543300	16695.8	8532.9	15721.3	15049.4	5375.6	10121.0
AY512827.1	106787	4978.2	1973.8	4839.3	4130.1	2100.8	2639.3
AY379977.1	97627	3715.6	2880.6	5981.6	7765.7	2280.5	3671.2
FM178827.1	332615	16021.1	8107.5	14995.6	14813.9	7075.9	7003.7
CU920294.1	542956	6644.8	3474.6	5612.4	8441.2	668.8	3036.4
NR_029001.1	568325	4773.9	4463.5	6890.7	4185.2	6163.1	5649.3
AY291121.1	99960	9931.3	5671.9	20488.9	15351.8	6578.8	8913.2
DQ054782.1	137154	3420.4	3343.6	6128.6	5750.5	2001.4	4089.3
EU801615.1	348067	5423.3	1969.0	13488.6	10281.4	774.8	2278.9
EU801564.1	356256	10633.1	3016.1	16805.4	14227.7	771.7	2346.5
EU800320.1	305174	13470.9	4558.9	23566.2	18391.5	2610.9	3314.9
EU800970.1	335155	11479.7	3092.5	19862.3	16434.7	630.7	2101.5
EU800733.1	321700	11083.2	3862.3	19817.3	16217.2	1391.4	3896.9
AY662014.1	137421	2597.3	1713.1	17820.2	13275.5	494.9	1347.7
EU800384.1	305775	12793.5	2358.0	9527.8	13523.4	1010.9	2592.8
DQ234121.2	143875	13160.5	3567.9	18226.6	15219.7	1290.9	3589.6
EF121352.1	206051	15439.1	8058.6	12215.1	14230.3	6678.5	7873.8
EU800631.1	346376	9060.0	4935.0	9116.0	13228.8	3244.2	3362.2
EU801033.1	330659	13662.7	4944.4	24351.9	18726.7	1691.8	4876.7
FN428768.1	535518	18530.1	7024.4	22476.4	16668.9	4586.6	8420.9
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EU801768.1	314723	9918.0	3954.9	11211.5	14491.2	5834.8	6008.5
EU801726.1	332065	9481.5	1611.2	6454.4	9320.3	1173.0	2278.4
FJ612396.1	582407	18709.5	2455.2	16355.9	12188.7	1704.4	3733.6
FN428758.1	567530	17355.3	5844.8	22738.0	16040.1	3936.8	6202.6
EU801561.1	332569	9255.6	2380.3	14988.1	14671.9	992.0	2235.8
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AY947947.1	141740	15460.4	6577.3	23169.0	18880.2	3059.1	7032.0
AY792257.1	124653	11306.5	6989.5	11164.6	13429.4	5208.0	7868.2
DQ501305.1	195239	5131.8	4963.1	8297.7	8943.3	3020.6	5129.9
EU801645.1	341378	16778.1	7383.9	23536.0	17988.5	7620.4	7609.7
AY948061.1	141397	18764.4	10666.0	27463.4	21096.6	7064.1	10616.1
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FJ612165.1	512885	15427.2	5958.5	15533.3	11124.3	2054.6	4513.2
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EF667919.1	250266	14523.3	9135.6	16695.9	14640.1	6735.6	9532.0
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g__Pelomonas
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s__Polaromonas aquatica	8413
s__Polaromonas naphthalenivorans	7660
s__Polaromonas sp. JS666	8802
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L33974.1 gg_id:7170 Leptothrix discophora str. SP-6
AM501440.1 gg_id:248405 Pelomonas puraquae str. CCUG52770 MG64
AF396932.1 gg_id:112368 Pseudomonas saccharophila str. PRO7
DQ884343.1 gg_id:170667 Pseudomonas sp. str. JS-1
AM039830.1 gg_id:133518 Polaromonas aquatica str. CCUG 39402
NC_008781.1 gg_id:194205 Polaromonas naphthalenivorans str. CJ2
AAFQ02000005.1 gg_id:129807 Polaromonas sp. str. JS666
DQ298150.1 gg_id:142773 -dependent and microbial assemblages silkworm midgut clone swm42
AB464945.2 gg_id:323641 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c
AF361203.1 gg_id:53922 mesoeutrophic reservoir clone 16
AY166684.1 gg_id:76891 Polaromonas naphthalenivorans str. CJ2
U14585.1 gg_id:7005 Polaromonas vacuolata str. 34-P
DQ341420.1 gg_id:150971 Acidovorax sp. str. Antarctic IS08
AF407386.1 gg_id:33769 MCB-contaminated groundwater-treating reactor clone RB7C8
AB252078.1 gg_id:152145 entrapped Puruogangri ice core clone PIC-D3
EU801289.1 gg_id:323062 It's all ranking aquatic Chesapeake Bay MD clone 3C002543
EU636027.1 gg_id:278933 Antarctic str. G020
EU636024.1 gg_id:279595 Antarctic str. G076
AY218637.1 gg_id:81748 penguin droppings sediments clone KD4-57
EU636029.1 gg_id:278079 Antarctic str. G088
FJ979854.1 gg_id:384326 Polaromonas sp. str. tsz24
FJ801199.1 gg_id:552577 Investigation Water -DGGE and Clone Library Zoige Alpine Wetland clone ZWB3-18
EU030285.1 gg_id:254221 Polaromonas jejuensis str. JS12-13
EU801930.1 gg_id:355065 It's all ranking aquatic Chesapeake Bay MD clone 3C003311
EF423322.1 gg_id:212990 Polaromonas sp. str. 1006
EU703261.1 gg_id:448038 lakes on Eastern Tin Plateau oligosaline lake altitude 4718 masl clone XZNMC60
DQ094183.1 gg_id:130292 Polaromonas sp. 'hydrogenovorans' str. hydrogenovorans
EU636028.1 gg_id:279079 Antarctic str. CC10
AY188325.1 gg_id:79327 penguin droppings sediment clone KD7-99
FM161402.1 gg_id:291214 Polaromonas sp. str. 01WB02.3-26
AB167243.1 gg_id:107951 str. c115
AY168739.1 gg_id:75143 arsenite-oxidizing biofilm clone HC-3
GU213397.1 gg_id:540184 Polaromonas sp. str. 190
EF516819.1 gg_id:224825 grassland soil clone FCPN433
GU208230.1 gg_id:588612 Study on Sediment Dongping Lake sediment clone 3S4-1
AY921863.1 gg_id:113128 farm soil clone AKYH1084
EU881341.1 gg_id:340905 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
DQ984611.1 gg_id:237973 LY oil-contaminated soil clone LYC180
GQ079635.1 gg_id:390755 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232d(
AY439189.1 gg_id:104669 soil clone MeCl 24
AJ532684.1 gg_id:76621 uranium mill tailings clone Gitt-KF-21

L33974.1	7170	13710.4	7718.7	21195.9	14342.7	7224.3	10734.0
AM501440.1	248405	5726.0	3352.1	17733.7	9675.4	4190.2	6861.3
AF396932.1	112368	3588.9	3539.6	4938.9	4723.1	4254.9	6910.6
DQ884343.1	170667	9967.7	4674.3	8861.9	7091.6	4055.5	5830.7
AM039830.1	133518	4569.1	3309.8	11003.1	8626.9	1914.3	3119.1
NC_008781.1	194205	1786.8	453.5	1252.2	2909.6	457.5	2079.1
AAFQ02000005.1	129807	2688.4	3335.1	19403.0	9103.4	1793.2	3057.5
DQ298150.1	142773	7309.9	5492.1	8291.0	8493.0	10210.3	8850.6
AB464945.2	323641	1776.4	2203.1	5405.1	1926.2	5663.4	4221.0
AF361203.1	53922	936.2	823.6	903.0	1560.8	312.5	575.7
AY166684.1	76891	10127.2	2724.6	6905.1	7929.2	2524.1	5232.6
U14585.1	7005	2775.9	3786.4	11420.4	7425.7	6239.7	2183.0
DQ341420.1	150971	777.9	273.0	1142.7	1291.7	1173.4	2638.6
AF407386.1	33769	8181.8	5946.5	15281.1	13577.1	4580.4	6351.2
AB252078.1	152145	5296.3	1691.8	2413.6	6285.9	470.9	1720.2
EU801289.1	323062	7479.5	1685.0	10378.0	5531.8	439.0	1129.0
EU636027.1	278933	9181.6	4313.9	13428.6	10283.1	2605.6	4218.5
EU636024.1	279595	8382.9	3450.5	8665.7	9786.9	3076.9	5692.5
AY218637.1	81748	9697.3	5684.0	13620.3	11571.0	3725.2	7391.1
EU636029.1	278079	6249.7	2385.0	10607.6	5533.1	2029.7	3168.7
FJ979854.1	384326	12932.7	8199.3	13136.6	12413.5	4213.6	6913.9
FJ801199.1	552577	6154.5	2330.9	7974.5	7249.4	1769.6	3073.6
EU030285.1	254221	5860.2	2692.4	9312.0	9845.1	1717.9	2581.3
EU801930.1	355065	12185.4	6750.2	15378.2	12806.2	6609.5	4969.6
EF423322.1	212990	9590.2	6407.3	20173.4	14181.3	5059.8	5886.2
EU703261.1	448038	2207.8	2155.6	7945.7	4378.6	1453.7	1876.4
DQ094183.1	130292	6755.6	3745.6	5211.5	8586.8	4118.3	4572.4
EU636028.1	279079	14507.6	5978.2	16101.7	14437.1	4952.9	7783.2
AY188325.1	79327	12129.2	9463.1	13467.5	14047.5	9151.5	12365.1
FM161402.1	291214	13726.0	7112.4	11981.9	14579.6	5357.0	8870.7
AB167243.1	107951	3548.9	1870.2	14413.5	9011.7	750.1	2585.9
AY168739.1	75143	14037.8	9182.4	9932.1	11519.4	7887.7	10213.9
GU213397.1	540184	9268.1	4536.2	15637.0	13181.2	5056.0	4578.4
EF516819.1	224825	7951.4	6118.4	10333.6	10409.8	4804.7	7633.1
GU208230.1	588612	4506.3	2667.4	4395.1	7228.3	3011.0	4503.6
AY921863.1	113128	4074.6	3934.4	8139.0	7430.2	4693.2	5387.3
EU881341.1	340905	6027.5	5023.8	7559.0	5973.4	3972.7	4404.2
DQ984611.1	237973	1570.1	1726.6	3684.6	4639.2	939.8	1246.0
GQ079635.1	390755	13711.7	5541.4	15162.8	11982.4	1754.1	3347.0
AY439189.1	104669	18726.2	9553.6	21224.8	17113.5	7586.1	10531.5
AJ532684.1	76621	16475.7	14813.3	6987.3	13927.7	14052.8	12072.9

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DQ354711.1 gg_id:154792 subsurface water clone DR550SWSAEE7
EF516224.1 gg_id:221803 grassland soil clone FCPU687
AB487846.1 gg_id:591765 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
FJ478510.1 gg_id:578098 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ451482.1 gg_id:156693 forest soil clone FAC43
EU979062.1 gg_id:317424 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
FM178814.1 gg_id:343929 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu
NC_007908.1 gg_id:153264 Rhodoferax ferrireducens str. DSM 15236
D16212.1 gg_id:6979 Rhodoferax fermentans str. FR3
X95837.1 gg_id:6986 situ visualization genetic natural microbial ecies strain T3
FJ517716.1 gg_id:513243 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e
AY214178.1 gg_id:82365 benzene-contaminated groundwater clone ZZ9C20
DQ628924.1 gg_id:162964 sequences Arctic glacier subglacial water ice or sediment clone SIB1 2B
DQ856540.1 gg_id:254818 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2M
AJ606333.1 gg_id:100951 Comamonadaceae SB1
DQ628925.1 gg_id:170859 sequences Arctic glacier subglacial water ice or sediment clone SIB2 1D
AB199580.1 gg_id:110990 river water Japan clone RVW-13
EU907895.1 gg_id:315915 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v
AY218635.1 gg_id:81515 penguin droppings sediments clone KD4-45
AF418942.1 gg_id:43083 USA: Colorado Fort collins Horsetooth Reservoir clone HTA10
EF203797.1 gg_id:236168 Chlorochromatium aggregatum
AB154311.1 gg_id:104501 freshwater clone S9F-53
EF451646.1 gg_id:216339 Rhodoferax sp. str. KAR16
EF580989.1 gg_id:278249 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM7
AJ421912.2 gg_id:27768 Germany:Elbe River clone Elb08
EF516373.1 gg_id:224371 grassland soil clone FCPT660
AB237669.1 gg_id:140742 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW
EU937983.1 gg_id:333026 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AJ867929.1 gg_id:142024 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone D8
EU937978.1 gg_id:330894 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
EU937973.1 gg_id:303742 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
EU104042.1 gg_id:353830 Evidence Comamonadaceae determinants settling performance activated sludge clo
GU233447.1 gg_id:516603 Rhodoferax antarcticus str. ANT.BR
CU466889.1 gg_id:338390 Evry wastewater treatment plant anoxic basin clone
AB475015.1 gg_id:566864 sequences located Engiadina Bassa Valley Switzerland iron containing freshwater so
AY214173.1 gg_id:81368 benzene-contaminated groundwater clone ZZ9C2
AB478658.1 gg_id:534216 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland clo
AB504936.1 gg_id:552998 structure microorganisms reddish-brown iron-rich snow clone oze05B33
GQ340212.1 gg_id:552309 Prokaryotic Marathonas Reservoir Greece water column clone VE07-26-BAC
EF580979.1 gg_id:279495 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1

FJ444709.1	578829	6676.3	5875.0	6549.7	6708.7	5464.9	5672.2
DQ354711.1	154792	1603.8	1628.3	3498.8	2154.4	466.8	1470.2
EF516224.1	221803	2604.6	296.6	846.1	1644.8	155.3	230.9
AB487846.1	591765	8174.8	8434.5	9678.1	8716.6	10387.4	8091.5
FJ478510.1	578098	3526.3	2397.8	5874.1	2291.0	2313.4	1498.1
DQ451482.1	156693	5646.2	5114.9	6274.9	7558.1	2845.3	3808.5
EU979062.1	317424	10996.4	6166.1	10546.3	9344.0	4205.0	6948.2
FM178814.1	343929	19551.5	6892.4	9536.4	11878.4	8062.9	8174.2
NC_007908.1	153264	8248.9	6493.0	17859.0	14635.4	3880.5	6234.2
D16212.1	6979	12159.6	7164.6	15482.8	14832.2	5697.2	7249.6
X95837.1	6986	11810.2	11654.7	22782.7	15828.7	11627.4	12895.6
FJ517716.1	513243	4220.9	4785.5	23766.3	14113.9	2072.2	4602.7
AY214178.1	82365	18005.5	12261.2	15351.2	16326.9	11998.5	12738.2
DQ628924.1	162964	8436.0	5988.1	13428.4	12625.1	3454.7	6598.6
DQ856540.1	254818	7244.7	5353.4	15904.9	10961.5	2851.9	3788.2
AJ606333.1	100951	3933.4	3750.5	4583.8	4886.4	2504.6	4071.6
DQ628925.1	170859	10804.1	6676.2	15749.0	17336.8	3677.1	6247.7
AB199580.1	110990	9518.7	7536.7	11050.3	12658.4	5254.8	6617.5
EU907895.1	315915	11020.3	5840.1	18116.1	13964.0	2180.2	6369.1
AY218635.1	81515	5960.3	3450.1	19081.6	14650.1	1178.9	3863.4
AF418942.1	43083	6865.9	5596.5	13890.8	8313.8	7485.7	7556.3
EF203797.1	236168	189.4	151.2	362.5	315.6	477.9	211.4
AB154311.1	104501	12846.6	7929.9	16382.8	15649.7	4295.1	6600.1
EF451646.1	216339	12615.3	6926.1	21202.5	17333.8	3442.9	6932.3
EF580989.1	278249	7612.3	4560.6	17181.0	11931.4	2141.9	3320.8
AJ421912.2	27768	6899.7	4074.6	12726.0	12008.5	3338.8	5703.6
EF516373.1	224371	19403.6	12760.8	18883.2	18310.9	12648.3	12156.9
AB237669.1	140742	7420.4	3779.2	6797.5	8288.5	969.3	3295.6
EU937983.1	333026	11974.6	9818.5	25900.2	19378.5	6952.4	9038.6
AJ867929.1	142024	9253.4	2512.0	16914.1	9488.4	1878.5	1847.5
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EU937973.1	303742	10342.8	4987.4	12606.8	14928.4	4679.7	5627.3
EU104042.1	353830	6678.5	5992.7	19835.6	11975.1	4000.1	4739.8
GU233447.1	516603	7276.8	3339.4	7859.0	12015.8	1042.7	3181.7
CU466889.1	338390	8403.2	4596.2	11218.6	11407.7	2889.7	5776.5
AB475015.1	566864	10597.1	4935.8	10884.8	11855.4	2276.1	4139.1
AY214173.1	81368	9340.4	3768.1	9975.0	9951.4	2733.6	4257.5
AB478658.1	534216	11170.1	3952.5	10268.5	11703.1	919.7	3354.4
AB504936.1	552998	7592.7	3248.8	11759.4	9848.3	1286.3	3723.5
GQ340212.1	552309	16643.5	3309.6	23944.6	14950.1	1369.0	3640.9
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AF435948.2 gg_id:75345 Rhodoferax ferrireducens str. T118
EF520458.1 gg_id:233033 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-15
AJ422168.1 gg_id:34909 Germany:Spittelwasser River clone Spb249
AB475020.1 gg_id:534700 sequences located Engiadina Bassa Valley Switzerland iron containing freshwater sou
CU466882.1 gg_id:347539 Evry wastewater treatment plant anoxic basin clone
EU340210.1 gg_id:248312 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
AY013643.2 gg_id:23857 sample taken downstream landfill clone BVB72 landfill
AY050600.1 gg_id:34176 MCB-contaminated groundwater-treating reactor clone GOUTB17
AF523029.1 gg_id:88367 natural mineral water clone G-5
EU104076.1 gg_id:340208 Evidence Comamonadaceae determinants settling performance activated sludge clo
AM697182.1 gg_id:222656 sequencing libraries indoor dust clone BF0001C023
FM955857.1 gg_id:581777 Rhodoferax sp. str. Asd M2A1
FJ437765.1 gg_id:546951 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa
DQ628926.1 gg_id:171241 sequences Arctic glacier subglacial water ice or sediment clone SIB2 10G
GQ339123.1 gg_id:526119 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
AJ867927.1 gg_id:144785 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone D6
EF590026.2 gg_id:231559 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
AJ421940.2 gg_id:20142 Germany:Elbe River clone Elb270
EU801480.1 gg_id:325766 It's all ranking aquatic Chesapeake Bay MD clone 3C002783
GQ389172.1 gg_id:587804 quality deterioration drinking system during serious red water outbreak clone D42
AJ421927.2 gg_id:20305 Germany:Elbe River clone Elb154
AF523038.1 gg_id:90178 natural mineral water clone H-5
EU104187.1 gg_id:331535 Evidence Comamonadaceae determinants settling performance activated sludge clo
DQ228371.1 gg_id:144642 microbial compositions two subglacial possible role microbes chemical weathering p
EU499697.1 gg_id:263522 Field-based laboratory stable isotope probing surveys identities both aerobic and an
AB475018.1 gg_id:542491 sequences located Engiadina Bassa Valley Switzerland iron containing freshwater sou
EF520463.1 gg_id:231370 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-46
EF590046.2 gg_id:230607 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
EU636030.1 gg_id:278005 Antarctic str. G079
DQ227795.1 gg_id:142898 Rhodoferax sp. PIC-C33
AJ421938.2 gg_id:18730 Germany:Elbe River clone Elb263
DQ664242.1 gg_id:172764 Rhodoferax sp. str. IMCC1723
DQ228394.1 gg_id:143719 microbial compositions two subglacial possible role microbes chemical weathering p
DQ532326.1 gg_id:168650 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
AF407396.1 gg_id:50642 MCB-contaminated groundwater-treating reactor clone RB9C6
CU466916.1 gg_id:337770 Evry wastewater treatment plant anoxic basin clone
AF407412.1 gg_id:44459 MCB-contaminated groundwater-treating reactor clone RB13C6
AM935036.1 gg_id:546472 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY214181.1 gg_id:82413 benzene-contaminated groundwater clone ZZ12C5
DQ521494.1 gg_id:198759 Antarctic lake ice cover clone ANTLV1_G06

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AB475020.1	534700	8294.6	3362.2	9253.3	11751.0	1479.7	4129.3
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EU340210.1	248312	14803.2	6167.1	18953.4	16627.4	3120.6	6044.1
AY013643.2	23857	10366.5	6236.0	16854.0	12271.0	3102.7	6344.6
AY050600.1	34176	13604.4	4606.8	22242.3	15497.7	5058.5	6140.5
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GQ339123.1	526119	8255.2	4250.0	15969.2	12781.5	799.1	3365.4
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DQ228394.1	143719	13018.5	9227.8	14736.4	13722.2	10843.0	13826.9
DQ532326.1	168650	6159.0	3558.6	4673.9	8966.3	2344.3	5560.3
AF407396.1	50642	8204.6	2601.5	8658.1	8849.5	783.7	2223.9
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DQ521494.1	198759	15256.4	8618.6	19956.2	15657.4	5163.6	8602.4

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AB030614.1 gg_id:50786 groundwater clone 1016
EF516197.1 gg_id:227151 grassland soil clone FCPT420
CU918346.1 gg_id:543524 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU801168.1 gg_id:340336 It's all ranking aquatic Chesapeake Bay MD clone 3C002403
AF173821.1 gg_id:6994 Antarctic clone LB3-27
AM936046.1 gg_id:543204 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU636023.1 gg_id:277658 Antarctic str. CA1
EF520443.1 gg_id:230788 structure lakes: what controls ? acid-impacted lake clone ADK-BMe02-01
AB508900.1 gg_id:581899 Roseateles sp. str. TSH99
GQ030687.1 gg_id:456337 Topographical and Temporal Human Skin Microbiome skin palm clone nbw881e04c1
FJ981655.1 gg_id:572135 Flea Vectors Plague clone XC5
GQ078254.1 gg_id:430107 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
EU538391.1 gg_id:285518 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88c04
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GQ076200.1 gg_id:458952 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
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EU539663.1 gg_id:281031 profile human microbiota antecubital fossa (inner elbow) skin clone nbt243g05
EU730923.1 gg_id:329183 Mitsuaria chitosanitabida str. 162
AJ512945.1 gg_id:80077 Caenibacterium thermophilum str. N2-680
EF127603.1 gg_id:208255 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone EME093
CU927221.1 gg_id:549143 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CT574057.1 gg_id:151642 Evry municipal wastewater treatment plant clone 054F01_B_DI_P58
CR933282.1 gg_id:109578 Evry municipal wastewater treatment plant clone 061G11_B_SD_P93
AF422679.1 gg_id:37583 TCE-sediment clone d156
AY218554.1 gg_id:82194 penguin droppings sediments clone KD1-134
FJ982926.1 gg_id:422910 Simplicispira limi str. ST3
AF078755.1 gg_id:7088 Aquaspirillum psychrophilum str. LMG 5408
AY780904.1 gg_id:143192 Aquaspirillum metamorphum str. 416
Z93960.1 gg_id:7097 activated sludge clone T33
EU434565.1 gg_id:264466 Simplicispira sp. str. b29
EU652480.1 gg_id:278324 Simplicispira sp. str. JPB-3.01
AJ863381.1 gg_id:119723 poplar tree microcosm rhizosphere flooded clone 5RHF31
CU466844.1 gg_id:324604 Evry wastewater treatment plant anoxic basin clone
AJ863422.1 gg_id:126382 poplar tree microcosm rhizoplane flooded clone 23RPF1
DQ975218.1 gg_id:250332 Iron sulfide and pyrite potential electron donors microbial nitrate reduction fresh wa
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CU466876.1 gg_id:316181 Evry wastewater treatment plant anoxic basin clone
DQ640671.1 gg_id:233183 full-scale EBPR sludge clone Skagenf43
AY275432.1 gg_id:98380 Brachymonas petroleovorans str. CHX
GQ024888.1 gg_id:484782 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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AY218554.1	82194	10.7	32.9	54.9	34.0	55.3	42.5
FJ982926.1	422910	6121.5	2801.4	7007.5	8324.2	2291.0	3807.1
AF078755.1	7088	4672.8	3628.2	7807.3	10124.0	1468.2	4748.0
AY780904.1	143192	7838.6	4877.1	20240.0	12596.2	4293.0	5267.3
Z93960.1	7097	16537.1	9065.2	23006.5	16495.4	6147.6	9937.0
EU434565.1	264466	680.0	414.9	4918.7	6151.3	145.7	441.9
EU652480.1	278324	12109.0	8346.9	12466.5	13035.6	8295.9	8852.5
AJ863381.1	119723	9453.6	5759.9	10227.1	9931.1	4628.8	5841.6
CU466844.1	324604	12440.0	8360.6	11234.8	13713.3	8156.3	8289.4
AJ863422.1	126382	1725.3	1536.4	4304.0	3246.2	189.5	823.5
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FJ516827.1 gg_id:572684 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s
GQ102483.1 gg_id:433031 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
AF439400.1 gg_id:40752 Ramlibacter henchirensis str. TMB834
AM411934.1 gg_id:237073 Variovorax sp. str. P-34
GU208252.1 gg_id:590127 Study on Sediment Dongping Lake sediment clone 6S3-1
AF144383.3 gg_id:7037 Ramlibacter tataouinensis str. TTB310
FJ612171.1 gg_id:567473 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.4.83
EF520494.1 gg_id:230979 structure lakes: what controls ? acid-impacted lake clone ADK-WYe02-39
GQ022440.1 gg_id:487228 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ020798.1 gg_id:488871 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ264547.1 gg_id:141807 universal microarray broader than typical library when sampling subsurface groundv
EU978826.1 gg_id:544356 and metabolic potential metagenome glacier ice clone glb338c
FJ534997.1 gg_id:533886 Enhancement protein conversion volatile fatty acids accumulation during addition: ef
GQ089363.1 gg_id:407227 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
AJ565430.1 gg_id:89333 Hylemonella sp. WQH1
GQ059928.1 gg_id:403464 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
DQ234183.2 gg_id:142262 determined library mangrove clone DS100
GQ060097.1 gg_id:404459 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
EF520474.1 gg_id:230959 structure lakes: what controls ? acid-impacted lake clone ADK-HDh02-57
EU801607.1 gg_id:325206 It's all ranking aquatic Chesapeake Bay MD clone 3C002944
FJ484871.1 gg_id:569745 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
GQ038137.1 gg_id:404029 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu38
EU801055.1 gg_id:320222 It's all ranking aquatic Delaware Bay NJ clone 2C229356
GQ021512.1 gg_id:488156 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27
EU881143.1 gg_id:323551 Karst region primary forest soil clone KPF200711-105
EU652471.1 gg_id:279025 Pseudomonas sp. str. JPB-1.12
AB166668.1 gg_id:101184 Leptothrix sp. str. SAYI-C
AF234683.1 gg_id:38002 sludge clone A15
AJ867925.1 gg_id:143202 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone D4
DQ640667.1 gg_id:229779 full-scale EBPR sludge clone Skagenf97
GQ339130.1 gg_id:523295 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
DQ521517.1 gg_id:190163 Antarctic lake ice cover clone ANTLV2_E04
FM873335.1 gg_id:367349 occupant source house floor dust clone FD01H06
EF660749.1 gg_id:245337 Pelomonas soli str. SYB4
EF632937.1 gg_id:252287 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
CU466870.1 gg_id:344265 Evry wastewater treatment plant anoxic basin clone
AB114618.1 gg_id:103415 rice plant clone ER-50
EU542576.1 gg_id:258654 Ideonella sp. str. 1a22
AF293003.1 gg_id:37495 ferromanganous micronodule clone MNE12

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EF520494.1	230979	16805.8	5459.4	9859.0	15351.1	1072.7	4103.2
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EF520474.1	230959	11656.3	5817.5	10155.1	11915.7	2913.4	4403.2
EU801607.1	325206	7472.7	5348.2	11286.7	9119.4	2200.3	4393.7
FJ484871.1	569745	6662.4	3435.9	8297.4	9502.8	2175.1	4101.3
GQ038137.1	404029	8755.5	2664.4	7949.7	8936.9	2562.4	4463.4
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GQ021512.1	488156	10634.6	4863.2	13557.8	14002.3	4807.7	7701.2
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AB166668.1	101184	10585.8	12354.2	8028.0	9348.4	14137.9	12921.1
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AJ867925.1	143202	9963.3	7045.8	17904.7	11068.0	6723.6	8733.9
DQ640667.1	229779	15168.6	11293.3	18711.8	15690.8	11713.5	10594.2
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AJ422174.2 gg_id:23589 Germany:Spittelwasser River clone Spb283
DQ656489.1 gg_id:160616 Aquicola tertiaricarbonis str. L10
FJ517015.1 gg_id:538250 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
EU881220.1 gg_id:355367 Karst region natural restoration land soil clone KNR200711-005
DQ413070.1 gg_id:152813 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EF520457.1 gg_id:233054 structure lakes: what controls ? acid-impacted lake clone ADK-GRe02-95
AB252908.1 gg_id:173323 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 187
DQ413123.1 gg_id:153307 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EU528188.1 gg_id:282506 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
CU466856.1 gg_id:311170 Evry wastewater treatment plant anoxic basin clone
NR_024710.1 gg_id:561541 Pelomonas saccharophila str. DSM 654
DQ066963.1 gg_id:129997 Lake Washington sediment clone pLW-2
CU466911.1 gg_id:312297 Evry wastewater treatment plant anoxic basin clone
AY947999.1 gg_id:143722 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl
AY921693.1 gg_id:113507 farm soil clone AKYG1800
FJ612162.1 gg_id:576928 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.4.31
EU638506.1 gg_id:340339 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AB252904.1 gg_id:171114 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 233
AY212560.1 gg_id:102288 water 10 m downstream manure clone 109ds10
EF540425.1 gg_id:218435 oil-shale semi-coke solid waste clone MK4a
FJ484912.1 gg_id:561277 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat
DQ327690.1 gg_id:167798 Biological filtration limits carbon availability affects downstream biofilm formation a
DQ337559.1 gg_id:145288 Pseudomonas sp. BBCT8
AM990747.1 gg_id:278347 Leptothrix sp. MOLA 523
FJ902318.1 gg_id:541652 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal
FJ902628.1 gg_id:541372 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
AY212645.1 gg_id:107717 water 20 m upstream manure clone 192up
EU244077.1 gg_id:365878 16SrRNA probes river Leine sediment clone sls1359
AY947934.1 gg_id:143876 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
AB240317.1 gg_id:144929 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon
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AY622242.1 gg_id:106999 subsurface soil clone B-E7
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DQ066964.1 gg_id:130439 Lake Washington sediment clone pLW-3
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DQ241397.1 gg_id:143057 Leptothrix sp. str. S1.1
AB240488.1 gg_id:142529 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
EU340201.1 gg_id:250274 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
AF498703.1 gg_id:58127 soil isolate Ellin321
GQ093947.1 gg_id:404750 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

AF244133.1	45926	1596.9	1887.3	3843.6	3028.1	1755.7	3058.5
AJ422174.2	23589	7576.1	6082.0	9160.4	5625.5	4287.7	4562.9
DQ656489.1	160616	1288.0	1769.8	4945.4	2512.9	1155.3	2657.9
FJ517015.1	538250	498.9	1252.4	2247.7	1053.9	537.7	631.8
EU881220.1	355367	5711.0	4965.6	7567.5	6396.2	3930.9	7140.4
DQ413070.1	152813	2621.4	4182.1	3700.8	4497.6	2089.1	3652.8
EF520457.1	233054	12431.6	6595.9	10234.0	12323.9	5317.8	6932.1
AB252908.1	173323	1143.7	3317.1	6208.8	1632.0	829.7	943.2
DQ413123.1	153307	5800.7	5435.1	10552.0	9679.4	4017.6	6064.3
EU528188.1	282506	8283.9	7140.0	9937.2	7739.8	1205.8	3193.4
CU466856.1	311170	5411.4	3285.9	7372.7	6469.2	3947.9	4955.6
NR_024710.1	561541	8273.6	2438.8	7480.5	8369.5	6143.3	9406.0
DQ066963.1	129997	3846.9	5238.3	13239.8	7534.2	4028.2	3557.4
CU466911.1	312297	7655.6	8436.2	11665.0	9792.9	8200.2	11981.8
AY947999.1	143722	10871.1	9323.8	11427.5	9608.5	8722.7	7768.0
AY921693.1	113507	3053.7	4294.7	7111.5	1859.5	2469.4	2673.2
FJ612162.1	576928	10126.9	4213.6	16153.0	10867.2	2114.8	3370.0
EU638506.1	340339	2571.9	3488.3	4824.6	2741.6	2791.3	2574.4
AB252904.1	171114	6419.5	7942.0	12177.9	7324.1	4946.6	5753.5
AY212560.1	102288	18513.7	18135.4	13809.0	16998.5	17878.9	16855.9
EF540425.1	218435	3510.4	2282.7	4488.9	3982.1	1387.4	2575.1
FJ484912.1	561277	4212.4	3732.8	5583.5	3880.7	2812.3	3690.5
DQ327690.1	167798	1259.4	2388.0	8212.4	2142.5	4260.1	2739.3
DQ337559.1	145288	8822.3	3858.7	8531.2	6577.8	4295.7	6228.0
AM990747.1	278347	9192.9	4738.5	12835.5	9153.5	5836.4	5541.8
FJ902318.1	541652	2887.9	2272.8	4562.1	3966.0	1906.6	2718.6
FJ902628.1	541372	5202.7	5879.5	6833.7	6174.0	5993.2	5499.9
AY212645.1	107717	2370.6	3428.0	2934.3	2656.8	2975.1	2747.9
EU244077.1	365878	4144.5	3565.9	6993.2	4928.1	2160.5	2356.1
AY947934.1	143876	8537.5	7324.2	10461.7	9026.2	4551.8	6479.5
AB240317.1	144929	5674.7	5546.3	9225.2	6652.5	2898.7	5335.2
AF234681.1	48162	7031.3	7597.7	8644.1	7472.7	3632.5	6119.9
AY622242.1	106999	6437.7	3641.5	6176.0	6994.3	3819.2	4593.8
AB015048.1	7128	1709.8	1881.0	3335.7	1631.6	976.7	2393.7
DQ066964.1	130439	11930.6	7344.9	12230.5	9598.2	3026.6	6402.6
DQ017912.1	136963	3029.8	3598.3	4702.8	1704.5	1758.8	1522.3
DQ241397.1	143057	8912.1	9319.9	15352.7	9160.0	6895.5	8800.6
AB240488.1	142529	7544.7	6080.5	14513.2	10842.7	4716.8	5787.0
EU340201.1	250274	5530.9	5324.6	7735.0	7559.9	3718.4	4167.6
AF498703.1	58127	6312.2	4270.6	8938.7	11708.3	4534.9	3659.1
GQ093947.1	404750	6533.9	4620.2	8055.3	8844.6	2610.0	4977.4

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AF368755.1 gg_id:19861 Pseudomonas saccharophila str. 5-1
AF234685.1 gg_id:17679 sludge clone A26b
FJ478604.1 gg_id:581639 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF079081.1 gg_id:244828 seeps sulfur-rich neutral pH ecosystem ochre-colored flocculent iron seep ditch fresh
AB240526.1 gg_id:144416 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
CU466896.1 gg_id:355908 Evry wastewater treatment plant anoxic basin clone
FJ152778.1 gg_id:341579 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
AM501430.1 gg_id:256189 Pelomonas saccharophila str. LMG2256
EU283393.1 gg_id:251129 consecutively aerated submerged treating domestic wastewater activated sludge m
AB480710.2 gg_id:556657 Leptothrix sp. str. PW5B
EU104010.1 gg_id:308805 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ402782.1 gg_id:557460 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ836752.1 gg_id:169856 attached biomass denitrifying bioreactor clone DB-14
CU466869.1 gg_id:333262 Evry wastewater treatment plant anoxic basin clone
X97071.1 gg_id:7126 Leptothrix mobilis str. Feox-1
AB271046.1 gg_id:172053 Leptothrix ginsengisoli str. Gsoil 1005
AY212570.1 gg_id:107290 water 10 m downstream manure clone 119ds10
CU466877.1 gg_id:305915 Evry wastewater treatment plant anoxic basin clone
EU015116.1 gg_id:243107 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
EU244040.1 gg_id:364166 16SrRNA probes river Leine sediment clone sl1288
AY947983.1 gg_id:143699 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
EU340184.1 gg_id:235584 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
AJ576389.1 gg_id:104905 midgut homogenate Pachnoda ephippiata larva clone PeM24
EU817495.1 gg_id:334185 Comamonas sp. str. XJ-L79
AY212575.1 gg_id:99071 water 10 m downstream manure clone 124ds10
FJ823942.1 gg_id:529615 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
EU801639.1 gg_id:342792 It's all ranking aquatic Chesapeake Bay MD clone 3C002983
EU488023.1 gg_id:545997 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
AM778004.1 gg_id:247071 nonsaline . Influence pore-size filters determination structure alkaline groundwater
AY768824.1 gg_id:108787 deep terrestrial fracture system clone D8A_4
DQ537534.1 gg_id:170339 manganese oxidation soil clone JH-GY34
GQ263735.1 gg_id:558043 Structure Simulated Level Waste Site simulated level waste site clone WC1_a51
DQ301787.1 gg_id:147885 Comamonas sp. str. PHD-10
DQ824571.1 gg_id:191875 human fecal clone RL185_aaj69g09
FJ009392.1 gg_id:305949 Hydrogenophaga intermedia str. C1
GQ404493.1 gg_id:588562 Hydrogenophaga flava str. ENV735
AB195168.1 gg_id:108779 Comamonas sp. str. 147S
AF280845.1 gg_id:21592 bioreactor clone mle1-6
AJ420328.1 gg_id:30654 Hydrogenophaga flava str. DSM 619
DQ202143.1 gg_id:139876 denitrifying treating groundwater contaminated nitrate and uranium fluidized bed r
EU037345.2 gg_id:261198 structure landfill sediments receiving long-term augmentations wastes chromium co

AF368755.1	19861	5733.5	3993.3	7292.2	7214.3	7628.8	9513.9
AF234685.1	17679	7969.3	8564.9	8873.9	8520.3	3006.3	5528.8
FJ478604.1	581639	8600.6	6859.5	8389.7	9782.4	11622.2	8931.0
EF079081.1	244828	4576.2	1530.1	4931.3	6179.7	3101.9	6399.0
AB240526.1	144416	7133.5	4393.1	6199.1	7759.7	3937.8	6363.5
CU466896.1	355908	2521.3	3213.7	8600.8	4827.0	2068.2	2736.0
FJ152778.1	341579	3420.8	3390.7	7483.4	5243.0	1959.4	2986.2
AM501430.1	256189	7036.3	2011.3	7538.8	7647.4	4732.2	8020.0
EU283393.1	251129	3984.1	5760.7	7269.7	4317.0	2535.0	4903.2
AB480710.2	556657	4855.5	4083.4	11580.2	11318.1	2615.7	5359.0
EU104010.1	308805	13123.8	6511.2	13034.0	15715.8	7593.7	9873.9
GQ402782.1	557460	3260.3	2943.0	6481.0	2985.3	1042.8	2790.8
DQ836752.1	169856	85.3	236.8	488.0	256.0	259.8	401.6
CU466869.1	333262	6892.6	7457.1	7925.0	9488.2	5799.4	6370.5
X97071.1	7126	9118.6	6746.4	11227.9	9423.3	10000.9	10134.6
AB271046.1	172053	1714.4	3244.0	9013.0	3330.2	1369.5	3768.0
AY212570.1	107290	4471.1	3564.4	4902.9	5726.4	3723.2	6020.6
CU466877.1	305915	4955.2	5530.6	10510.5	7069.9	6429.5	6683.2
EU015116.1	243107	7422.9	5110.8	9696.5	8573.5	3372.3	5024.0
EU244040.1	364166	4464.9	2820.4	5493.7	5630.5	2032.4	2489.7
AY947983.1	143699	2353.2	1252.3	3927.4	2572.9	1474.3	2057.0
EU340184.1	235584	10392.6	7147.4	11752.7	11038.1	4713.0	6760.2
AJ576389.1	104905	22.5	63.9	44.4	53.6	106.7	230.6
EU817495.1	334185	4278.8	4028.7	10336.8	6790.5	5096.8	7026.9
AY212575.1	99071	10020.2	7672.6	12587.5	14341.2	8614.9	11276.9
FJ823942.1	529615	5534.8	2259.7	8384.8	5503.0	2789.0	4042.6
EU801639.1	342792	10304.8	8600.0	18497.4	13489.1	4958.6	8741.0
EU488023.1	545997	6807.3	8128.0	9896.9	6319.9	9246.3	8584.6
AM778004.1	247071	4550.4	2715.5	5382.7	6880.5	1885.6	3225.1
AY768824.1	108787	4727.1	2503.0	4025.0	5508.5	1511.5	3181.9
DQ537534.1	170339	186.4	229.1	91.4	155.6	193.7	150.4
GQ263735.1	558043	6650.4	3204.9	8355.2	8364.4	5558.4	6434.4
DQ301787.1	147885	12149.9	4067.6	11989.7	11360.9	1799.8	5741.9
DQ824571.1	191875	7317.6	2987.9	7991.6	6920.5	4868.3	3793.3
FJ009392.1	305949	12015.3	8217.3	13078.4	13363.1	8463.9	11107.1
GQ404493.1	588562	4988.9	3327.6	5749.3	7922.3	2838.3	4914.5
AB195168.1	108779	3235.7	1586.8	5369.1	5185.1	909.1	3112.4
AF280845.1	21592	7352.0	6450.1	8399.4	9120.9	6781.2	7698.2
AJ420328.1	30654	6561.6	5701.4	4982.0	6420.2	2947.8	4352.5
DQ202143.1	139876	5322.9	4451.2	9859.3	10181.4	1387.0	3894.4
EU037345.2	261198	9727.6	5962.3	9174.2	11161.9	4181.0	3145.8

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DQ226086.1 gg_id:141299 subsurface water clone EV821FW101601SAC94
AY947980.1 gg_id:142570 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
DQ854970.1 gg_id:164474 Hydrogenophaga sp. str. GPTSA14
AF019037.1 gg_id:6953 Hydrogenophaga intermedia str. S1
AF508103.1 gg_id:66240 Variovorax paradoxus TG27
DQ256326.1 gg_id:141917 subsurface water clone EV818BHEB5102502DRLWq27f021
AM777949.1 gg_id:237044 nonsaline . Influence pore-size filters determination structure alkaline groundwater
DQ824747.1 gg_id:173960 human fecal clone RL185_aaj72f07
AB195164.1 gg_id:108969 Comamonas sp. str. PD-10t
AJ853614.1 gg_id:111232 landfill leachate clone GZKB122
AB294326.1 gg_id:204877 Microbial structure deep coal seem groundwater stream clone SWB15
DQ234232.2 gg_id:141836 determined library mangrove clone DS150
AY218568.1 gg_id:81130 penguin droppings sediments clone KD2-104
EU104128.1 gg_id:352511 Evidence Comamonadaceae determinants settling performance activated sludge clo
EF469609.1 gg_id:224686 Pseudacidovorax intermedius str. CC-CC21
EF580985.1 gg_id:279450 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM5
AY823974.1 gg_id:148639 Investigation Acetate-Fed Denitrifying Microbial Stable Isotope Probing Full-Cycle an
EU037911.1 gg_id:235933 Metabolic Profiles Microbial Chlorinated Pesticides Contaminated Sites Three Geogr
AJ585992.1 gg_id:97176 Hydrogenophaga atypica str. BSB 41.8
AB077037.1 gg_id:78049 Macromonas bipunctata str. IAM 14880
FJ382319.1 gg_id:572939 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
AY863093.1 gg_id:112155 wastewater treatment pool clone SXAU055
DQ337093.1 gg_id:146820 subsurface water clone EV818SWSAP75
DQ824754.1 gg_id:184303 human fecal clone RL185_aaj72g06
AY947966.1 gg_id:141254 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
Z93993.1 gg_id:6940 activated sludge clone T60
FJ598354.1 gg_id:552978 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCWP1
AM110076.2 gg_id:250992 Hydrogenophaga sp. str. Rs71
AM042694.1 gg_id:161866 Tepidimonas thermarum str. AA2
AM777993.1 gg_id:251137 nonsaline . Influence pore-size filters determination structure alkaline groundwater
AB271047.1 gg_id:171214 Hydrogenophaga sp. str. Gsoil 1545
EF532793.1 gg_id:227420 Hydrogenophaga bisanensis str. K102
FJ660572.1 gg_id:561367 Correlation functional stability and dynamics full-scale wastewater treatment plant a
GQ114408.1 gg_id:418439 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
AF208386.1 gg_id:28592 Variovorax paradoxus str. WP1
AY212671.1 gg_id:104415 water 20 m downstream manure clone 223ds20
DQ824567.1 gg_id:191848 human fecal clone RL185_aaj69g05
DQ349098.1 gg_id:148264 Variovorax limosa str. EMB320
GQ008933.1 gg_id:500732 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB162104.1 gg_id:132598 trphc Dntrfng Hrbrd Sbsrfc Uplnd Sl Imprvd Cltrblt uplnd sl
AF509578.1 gg_id:91935 intestine clone

DQ226086.1	141299	11732.9	7578.4	8049.5	11682.9	9023.1	9335.8
AY947980.1	142570	13159.2	8088.6	17750.3	14643.6	10535.1	7685.0
DQ854970.1	164474	9148.9	5279.1	9299.5	11318.7	4821.2	8940.6
AF019037.1	6953	5450.9	3482.4	11053.4	9444.3	2164.3	6970.3
AF508103.1	66240	2075.7	1292.4	7386.8	6007.5	835.5	1226.2
DQ256326.1	141917	10451.5	2765.8	9351.8	9887.7	2312.8	5276.3
AM777949.1	237044	4878.8	5228.1	8638.3	9032.3	3613.3	5934.5
DQ824747.1	173960	14806.4	5433.7	9832.1	8156.5	8373.3	10120.1
AB195164.1	108969	8604.0	6534.8	8299.6	8386.9	6022.9	8194.7
AJ853614.1	111232	8173.0	6203.3	17071.2	14680.8	5316.4	7088.3
AB294326.1	204877	2517.5	2304.1	3639.3	7077.3	2740.6	4462.8
DQ234232.2	141836	8003.3	5248.6	10288.0	7773.0	7269.8	7531.3
AY218568.1	81130	3909.6	2860.2	6677.0	6314.1	6189.5	7060.9
EU104128.1	352511	6263.6	4588.5	9156.0	7239.4	4074.0	4929.8
EF469609.1	224686	10282.5	6461.1	13216.4	12670.2	4654.8	8806.5
EF580985.1	279450	11217.0	8413.8	14644.2	12996.7	7184.3	10010.5
AY823974.1	148639	18724.5	8563.9	19954.7	17408.3	4743.4	7119.7
EU037911.1	235933	8955.2	4716.3	9379.5	11625.7	2994.6	4612.7
AJ585992.1	97176	6131.8	2171.0	10624.9	7455.9	1090.3	4844.6
AB077037.1	78049	7392.0	5978.1	7823.1	4729.3	1923.3	3149.9
FJ382319.1	572939	6713.5	4564.0	4336.8	4822.2	4373.8	4379.1
AY863093.1	112155	10320.0	6762.5	4630.8	6634.3	7860.1	7645.6
DQ337093.1	146820	5161.6	2194.8	3126.6	8603.3	1243.0	2499.9
DQ824754.1	184303	5689.0	3526.3	5274.3	4250.7	4367.7	5772.0
AY947966.1	141254	7353.9	4864.0	7855.9	12346.7	1428.1	3924.8
Z93993.1	6940	5622.3	1230.0	1964.5	4622.7	321.2	801.1
FJ598354.1	552978	14882.8	13405.3	11237.8	15644.7	11924.5	12158.5
AM110076.2	250992	8353.5	5072.4	9754.3	9857.1	2175.4	4342.1
AM042694.1	161866	9832.5	5928.7	8872.8	10834.8	4660.6	6683.9
AM777993.1	251137	3642.4	3706.5	2225.2	6481.4	5601.2	6375.9
AB271047.1	171214	11344.5	4883.3	16495.7	11717.7	3422.1	7117.9
EF532793.1	227420	12933.8	5770.0	18731.6	9678.8	5711.0	8502.2
FJ660572.1	561367	11089.5	5644.1	9154.2	10847.2	3009.0	6361.0
GQ114408.1	418439	1235.3	218.3	2918.3	2792.2	334.7	971.9
AF208386.1	28592	15180.7	5320.7	10153.5	15489.6	2358.4	3378.7
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AB162104.1	132598	9436.4	5335.7	21502.9	13193.3	4909.1	4904.9
AF509578.1	91935	980.8	666.5	2252.7	866.4	692.1	1932.2

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EU104328.1 gg_id:306757 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ105163.1 gg_id:452868 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw!
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AF143840.1 gg_id:17198 hydrocarbon-degrading consortium clone AF1-8
GQ022589.1 gg_id:487080 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
AJ420330.1 gg_id:22998 Xylophilus ampelinus str. DSM 7250
EU834792.1 gg_id:512974 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se
GQ098554.1 gg_id:393420 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw703e
GQ076351.1 gg_id:444338 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
AB473892.1 gg_id:574956 sequences Cadagno di Fuori biofilm mat alpine wetland varying conductivities clone
EF520476.1 gg_id:232460 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-32
EU800578.1 gg_id:356291 It's all ranking aquatic Delaware Bay NJ clone 2C228724
AF445694.1 gg_id:38957 travertine hot spring clone SM1F12
AY622243.1 gg_id:107152 subsurface soil clone B-H11
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GQ059902.1 gg_id:450072 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ023366.1 gg_id:486307 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317e09
EU803910.1 gg_id:347702 It's all ranking aquatic Lake Gatun clone 5C231566
GQ023762.1 gg_id:485907 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
EU801997.1 gg_id:315609 It's all ranking aquatic Chesapeake Bay MD clone 3C003382
GQ019127.1 gg_id:490540 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
AY957923.1 gg_id:115132 drinking water biofilm clone B3NR69D8
GQ115248.1 gg_id:465653 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU817491.1 gg_id:337173 Acidovorax sp. str. XJ-L63
AY328735.1 gg_id:90243 drinking water system simulator clone DSSD36
EF516044.1 gg_id:226128 grassland soil clone FCPT659
GQ102413.1 gg_id:424237 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
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GQ023504.1 gg_id:486165 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319d08
GQ022778.1 gg_id:486891 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
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GQ023840.1 gg_id:485830 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
AB286633.1 gg_id:208284 Reducing production and domination comamonadaceae reducing oxygen supply was
GQ102613.1 gg_id:464509 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ114833.1 gg_id:394958 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ023964.1 gg_id:485707 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu

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GQ105163.1	452868	8274.9	6240.4	9252.9	11877.1	6566.7	8167.7
GQ020800.1	488868	16036.1	11728.5	9796.6	15530.4	12923.0	11817.8
AF143840.1	17198	19519.8	16308.7	17065.2	18936.4	16456.9	15147.5
GQ022589.1	487080	9218.5	5881.5	9634.7	9063.5	6449.1	6500.9
AJ420330.1	22998	5996.5	4789.2	13122.4	10668.0	3710.8	4391.0
EU834792.1	512974	5354.8	2673.7	9016.4	7372.4	1681.5	2808.4
GQ098554.1	393420	6988.1	4055.1	8997.2	8035.9	4832.7	6151.8
GQ076351.1	444338	5580.8	2141.2	8504.5	6775.4	1878.5	4572.4
AB473892.1	574956	7104.5	5595.1	10334.7	10255.4	1199.2	3157.0
EF520476.1	232460	8481.4	6435.6	15175.7	14478.6	4386.3	6559.2
EU800578.1	356291	8664.5	4005.8	11534.7	11269.4	1977.9	4674.7
AF445694.1	38957	9758.1	5579.6	16048.6	10602.8	4692.8	7795.6
AY622243.1	107152	6052.9	5917.2	6876.5	8617.1	6569.8	7670.7
GQ109099.1	417794	6641.0	3404.2	9740.8	8402.7	2850.5	5182.3
GQ059902.1	450072	16654.4	8133.1	20063.0	15471.2	7889.1	11492.9
GQ023366.1	486307	7789.9	7588.7	8043.6	9125.6	9242.7	7920.7
EU803910.1	347702	5043.6	3331.8	13367.9	10961.9	6570.1	3413.1
GQ023762.1	485907	10602.0	8765.4	9719.1	10659.5	9482.1	9808.3
EU801997.1	315609	6372.3	4652.2	23423.4	15425.5	2150.0	3678.7
GQ019127.1	490540	7865.2	3798.6	9153.1	9042.7	3779.4	5694.2
AY957923.1	115132	5267.0	5838.7	6891.0	5702.2	3861.6	5756.6
GQ115248.1	465653	10992.9	8263.2	8975.4	11275.0	11114.4	11308.3
EU817491.1	337173	2089.7	2277.6	4788.8	1878.2	2182.9	2500.7
AY328735.1	90243	557.9	574.4	1866.3	2356.8	286.9	793.8
EF516044.1	226128	3770.4	1870.9	4585.4	5453.6	1230.5	2198.2
GQ102413.1	424237	8902.6	6209.5	4983.7	11097.0	8803.3	9142.2
AY861870.1	112550	16176.8	9881.4	12025.8	16955.4	10256.2	11836.9
GQ023504.1	486165	9361.8	3759.0	10306.4	10406.7	2500.2	5290.1
GQ022778.1	486891	4961.5	2540.2	7499.1	7525.9	2735.5	4830.0
GQ102567.1	445839	12404.5	7149.1	13871.4	14141.4	7231.8	9630.6
GQ023840.1	485830	10396.2	3508.4	9348.6	9890.5	3216.2	5674.4
AB286633.1	208284	9276.8	6559.6	15398.5	14069.2	4570.3	6683.2
GQ102613.1	464509	9788.7	3604.1	9320.9	9424.3	3819.3	6174.7
GQ008571.1	501094	8293.2	4631.3	12673.7	10199.2	4747.2	7514.8
AY770420.1	128171	11046.8	5702.2	20416.4	17634.3	3765.2	9287.7
GQ023204.1	486465	14982.0	16439.1	13157.4	15519.0	13464.2	14445.4
GQ114833.1	394958	6866.2	2763.2	8908.7	10721.5	2536.1	6892.4
GQ008077.1	501590	13962.0	10056.1	12105.2	17145.4	9958.6	11196.8
GQ023964.1	485707	6361.3	3386.8	5853.0	7594.2	3100.7	5018.3

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DQ228365.1 gg_id:141075 microbial compositions two subglacial possible role microbes chemical weathering p
AM697584.1 gg_id:223416 sequencing libraries indoor dust clone BF0002D095
DQ501302.1 gg_id:194785 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw
EU799088.1 gg_id:316265 It's all ranking aquatic Newport Harbour RI clone 1C226647
GQ115389.1 gg_id:458026 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ086489.1 gg_id:459995 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29
GQ085322.1 gg_id:433672 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273h12(
DQ450189.1 gg_id:152484 (Uruguay) Atlantic coastal lagoon clone RS62
AY622262.1 gg_id:99188 subsurface soil clone B-BI94
EU287088.1 gg_id:245381 Pacific arctic surface sediment clone B78-124
AY212561.1 gg_id:102445 water 20 m upstream manure clone 10up
GQ090626.1 gg_id:387321 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
EU234306.1 gg_id:256947 penicillin G production wastewater receiving river and un techniques upstream Wan
EF520470.1 gg_id:227823 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-02
FJ535020.1 gg_id:589483 Enhancement protein conversion volatile fatty acids accumulation during addition: ef
EU937936.1 gg_id:320002 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
GQ100976.1 gg_id:389741 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48
EU800091.1 gg_id:344929 It's all ranking aquatic Delaware Bay NJ clone 2C228067
AY250104.1 gg_id:86368 napthalene-contaminated sediment clone 76
GQ113666.1 gg_id:431848 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ096134.1 gg_id:464571 Topographical and Temporal Human Skin Microbiome skin back clone nbw387b07c1
EF203185.1 gg_id:213853 phylotypes sediments Lake Kastoria Greece sediment clone Kas105B
EU589304.1 gg_id:262575 China Ningxia rice paddy field soil clone 2_E2
EU803706.1 gg_id:315287 It's all ranking aquatic Lake Gatun clone 5C231315
GQ340183.1 gg_id:564336 Prokaryotic Marathonas Reservoir Greece water column clone K07-73-BAC
EU800800.1 gg_id:326023 It's all ranking aquatic Delaware Bay NJ clone 2C229012
AB487042.1 gg_id:572462 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0(
EU800118.1 gg_id:324016 It's all ranking aquatic Delaware Bay NJ clone 2C228106
GQ103451.1 gg_id:442661 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
CU918086.1 gg_id:541772 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EF157142.1 gg_id:254138 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
GQ023051.1 gg_id:486618 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ101039.1 gg_id:384924 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48
EF562037.1 gg_id:247406 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
AB286619.1 gg_id:206338 Reducing production and domination comamonadaceae reducing oxygen supply was
EU801359.1 gg_id:354682 It's all ranking aquatic Chesapeake Bay MD clone 3C002625
AY102324.1 gg_id:65461 heavy metal-contaminated soil clone a13125
FJ612149.1 gg_id:586108 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.2.54
AB286606.1 gg_id:209495 Reducing production and domination comamonadaceae reducing oxygen supply was
GQ116352.1 gg_id:372613 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw691h02
GQ037265.1 gg_id:429168 Topographical and Temporal Human Skin Microbiome skin palm clone nbu391b06c1

DQ228365.1	141075	8562.5	3633.9	12019.6	10817.0	1758.0	3449.8
AM697584.1	223416	15520.3	9550.2	18916.5	17008.3	11164.5	9265.1
DQ501302.1	194785	8953.3	7202.7	17661.2	7190.3	9480.9	5381.8
EU799088.1	316265	13562.8	6490.1	19142.4	13872.3	6856.8	11247.3
GQ115389.1	458026	17478.6	16829.4	13274.5	15063.5	16953.3	15693.3
GQ086489.1	459995	3000.3	4602.1	5648.9	4515.1	3917.6	5671.8
GQ085322.1	433672	9214.0	3809.3	8032.9	9839.4	3818.9	5612.9
DQ450189.1	152484	11059.4	4114.8	9734.7	12679.9	3094.8	4925.2
AY622262.1	99188	4770.5	2787.6	12045.2	9009.8	1927.4	4637.8
EU287088.1	245381	13177.2	8696.5	16895.7	15667.0	7082.0	8921.5
AY212561.1	102445	4578.5	1446.3	16278.3	7333.1	2754.3	4864.3
GQ090626.1	387321	16917.7	7335.1	11468.3	17119.7	5023.0	8838.2
EU234306.1	256947	5726.4	2368.9	11721.7	6573.4	604.5	1626.0
EF520470.1	227823	794.9	343.6	2109.9	2101.3	259.7	484.5
FJ535020.1	589483	6095.2	2910.6	4036.7	8820.3	3369.5	4279.9
EU937936.1	320002	6881.4	6027.0	13290.6	9611.3	4657.7	4611.0
GQ100976.1	389741	4758.6	5539.1	11460.2	7467.0	8479.4	9605.1
EU800091.1	344929	5062.7	5831.2	14806.6	9919.8	2962.8	6876.3
AY250104.1	86368	6020.6	2248.4	7086.9	8552.5	1983.2	6118.3
GQ113666.1	431848	12114.2	7839.2	12974.2	11617.4	7940.8	9364.4
GQ096134.1	464571	10056.2	4877.7	9385.1	9951.7	5133.0	7013.8
EF203185.1	213853	4512.4	3209.2	5602.7	10222.6	2893.2	3378.7
EU589304.1	262575	6510.4	2762.3	8354.9	7026.2	3672.4	4173.5
EU803706.1	315287	9093.4	4026.6	13213.4	10197.6	3284.8	4425.8
GQ340183.1	564336	11069.3	6468.4	13102.4	11590.6	6619.6	8176.6
EU800800.1	326023	6438.1	5156.7	15643.2	16372.5	3137.7	6981.8
AB487042.1	572462	516.8	414.8	2273.4	1494.5	184.8	622.5
EU800118.1	324016	6484.5	4957.7	8445.2	12928.0	7484.7	7048.5
GQ103451.1	442661	8352.0	2830.2	10097.1	8483.2	2442.5	4499.8
CU918086.1	541772	10577.7	4423.6	14645.3	13982.0	2852.8	4506.6
EF157142.1	254138	7431.4	4130.4	10890.1	10777.6	6099.5	5732.5
GQ023051.1	486618	9919.5	4791.6	9349.3	10057.6	6252.0	7470.5
GQ101039.1	384924	9093.4	4304.5	9656.7	9045.3	3437.3	5435.4
EF562037.1	247406	16090.1	4355.0	6574.0	12503.7	2448.9	4023.0
AB286619.1	206338	14218.4	5929.1	14867.6	16409.4	4006.9	6281.3
EU801359.1	354682	5908.4	1761.2	21850.4	13857.4	546.7	2232.9
AY102324.1	65461	10615.6	8502.5	10688.9	11871.9	8053.4	7288.7
FJ612149.1	586108	11118.0	6063.4	13908.4	12221.9	9426.9	8598.5
AB286606.1	209495	18511.6	10932.2	16836.1	20630.6	12389.5	11196.7
GQ116352.1	372613	9093.0	8326.8	9749.9	8420.2	8037.3	9840.8
GQ037265.1	429168	4640.8	1122.1	4992.2	7422.2	406.8	1712.4

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AY861814.1 gg_id:112662 Obsidian Pool prime community clone OPPB083
EF516381.1 gg_id:223622 grassland soil clone FCPS464
EF157145.1 gg_id:253142 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU104241.1 gg_id:351875 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ002349.1 gg_id:507313 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176d04
AB286592.1 gg_id:216359 Reducing production and domination comamonadaceae reducing oxygen supply was
GQ060015.1 gg_id:448535 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
AY566579.1 gg_id:108727 Acidovorax sp. str. PG-06
GQ102770.1 gg_id:457672 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EF492935.1 gg_id:255248 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EU015090.1 gg_id:239385 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
DQ451457.1 gg_id:156987 forest soil clone FAC18
EU803951.1 gg_id:349195 It's all ranking aquatic Lake Gatun clone 5C231617
GQ039298.1 gg_id:450995 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
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EU978837.1 gg_id:545465 and metabolic potential metagenome glacier ice clone glb349c
GQ075567.1 gg_id:446083 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ534986.1 gg_id:513449 Enhancement protein conversion volatile fatty acids accumulation during addition: ef
GQ101831.1 gg_id:397741 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw499g11c
CU918612.1 gg_id:539274 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ398882.1 gg_id:155033 24-D amended agricultural soil clone 7
DQ984534.1 gg_id:241827 FD oil-contaminated soil clone FD_17
AB166780.1 gg_id:107032 EBPR sludge clone UTFS-OF05-33-21
GQ105774.1 gg_id:449419 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
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DQ234145.2 gg_id:143702 determined library mangrove clone DS061
EU104038.1 gg_id:327197 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU800160.1 gg_id:353966 It's all ranking aquatic Delaware Bay NJ clone 2C228154
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GQ284468.1 gg_id:587567 Acidovorax sp. str. TSWCW24
GQ103103.1 gg_id:451643 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ038169.1 gg_id:390094 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu38
GQ113644.1 gg_id:449285 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ059938.1 gg_id:454896 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ047911.1 gg_id:385873 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138h11c
GQ025075.1 gg_id:456577 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
EU808776.1 gg_id:312672 chloraminated system Prospect Tank clone Pro_CL-100633_OTU-7
GQ098350.1 gg_id:379750 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558c
DQ298342.1 gg_id:155949 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos

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EF157145.1	253142	7310.5	3256.1	6261.0	7573.8	4081.3	3711.8
EU104241.1	351875	6387.0	5391.7	14510.4	12333.2	6338.3	5993.3
GQ002349.1	507313	10769.5	5302.1	14831.5	16260.7	4619.7	7412.2
AB286592.1	216359	8578.5	3436.6	6247.9	11900.2	5743.1	5348.2
GQ060015.1	448535	16914.1	7741.0	20727.1	17451.5	8219.9	9925.1
AY566579.1	108727	10265.1	5897.1	7339.0	11436.0	3640.1	7176.1
GQ102770.1	457672	21545.7	17944.5	16366.1	19024.0	19101.4	17083.3
EF492935.1	255248	14258.0	13822.1	14007.2	11986.6	13993.3	13426.8
EU015090.1	239385	7442.5	2540.6	9517.6	7928.1	1679.1	1677.1
DQ451457.1	156987	8563.7	5346.6	14909.1	13394.7	6398.8	8236.9
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GQ039298.1	450995	15257.7	4299.1	10282.0	12743.8	6833.5	5983.8
GQ008150.1	501515	12104.2	10962.7	8013.1	12506.7	13310.3	9150.3
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GQ075567.1	446083	8520.0	3885.7	8609.1	9122.4	4911.0	6452.1
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DQ398882.1	155033	3598.2	2025.2	7646.3	5516.4	1752.6	4174.1
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AB166780.1	107032	12164.1	7061.1	7448.0	14087.9	1542.9	3930.3
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EF020052.1	211171	3488.7	2073.2	2536.0	4779.7	2240.0	3266.8
GQ284468.1	587567	4217.0	2921.7	14602.3	8001.9	1745.0	2637.2
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GQ022931.1 gg_id:486738 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
EU801144.1 gg_id:342959 It's all ranking aquatic Delaware Bay NJ clone 2C229491
GQ037854.1 gg_id:372737 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ008577.1 gg_id:501089 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
EU735719.1 gg_id:348978 Biological Arsenic Remediation Project Groundwater Aquifer soil clone 2As11
GQ024544.1 gg_id:485126 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123f01c1
Z93972.1 gg_id:6958 activated sludge clone T19
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EU801192.1 gg_id:334983 It's all ranking aquatic Chesapeake Bay MD clone 3C002436
DQ230947.1 gg_id:144759 subsurface water clone NO27FW100501SAB47
AY947979.1 gg_id:144564 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
AY168733.2 gg_id:136160 Oxidizing Biofilms: Cultivation Approaches and Rates Arsenite Oxidation arsenite-oxi
GQ082954.1 gg_id:450051 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ017926.1 gg_id:137000 upland stream clone S-Rwb_36
GQ076185.1 gg_id:449255 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
EU907888.1 gg_id:306159 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v
GQ094377.1 gg_id:394271 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ105741.1 gg_id:438927 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
GQ098862.1 gg_id:436788 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558a
EU676430.1 gg_id:302458 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
GQ249361.1 gg_id:547824 Research on biodiversity sludge bioflim Biological Aeration Filter clone A17
EU800119.1 gg_id:341614 It's all ranking aquatic Delaware Bay NJ clone 2C228107
EU801154.1 gg_id:314075 It's all ranking aquatic Delaware Bay NJ clone 2C229504
EU735706.1 gg_id:337175 Biological Arsenic Remediation Project Groundwater Aquifer soil clone 1As18
AF502223.1 gg_id:59344 EBPR sludge lab scale clone HP1B35
EF516428.1 gg_id:220686 grassland soil clone FCPP550
GQ009720.1 gg_id:499945 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
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DQ432053.1 gg_id:154227 Variovorax koreensis str. GH 9-3
AY160868.1 gg_id:95932 termite intestinal tract clone COB P5-8
AJ420329.1 gg_id:35360 Variovorax paradoxus str. DSM 66
EU169184.1 gg_id:247107 Variovorax paradoxus str. B54
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DQ256486.1 gg_id:144358 Variovorax paradoxus Jm111
AB269775.1 gg_id:209527 Variovorax paradoxus str. HYK0512-SK12
EF641108.1 gg_id:279410 Variovorax paradoxus str. TBEA6
FJ214196.1 gg_id:342494 Co-speciation earthworms and their nephridial symbionts nephridia clone Ai3-13
FJ214173.1 gg_id:327535 Co-speciation earthworms and their nephridial symbionts nephridia clone Lf3-5
FJ214186.1 gg_id:315987 Verminephrobacter sp. str. At4
AJ543434.1 gg_id:83899 nephridia Octolasion lacteum clone Ol2-2

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EU801144.1	342959	7793.2	3943.8	6853.3	9914.6	1553.5	2671.4
GQ037854.1	372737	6873.8	4265.0	11630.8	9089.0	4038.3	7716.8
GQ008577.1	501089	16932.4	11306.6	16838.0	16598.4	10607.0	11516.6
EU735719.1	348978	6664.0	5315.7	11777.3	7563.9	5285.5	7759.3
GQ024544.1	485126	16708.4	6690.7	16716.2	15814.8	3494.5	3267.0
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EU104165.1	345705	9847.6	4940.1	9067.9	10341.6	5012.0	7022.1
EU801192.1	334983	17602.1	5936.2	16291.4	14870.4	7176.9	7075.4
DQ230947.1	144759	6746.3	4022.1	7926.1	10141.6	3281.4	5857.7
AY947979.1	144564	11106.8	6225.2	15339.8	13558.6	5191.5	6420.3
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GQ082954.1	450051	16792.6	16054.2	18675.1	16252.8	14976.9	14897.7
DQ017926.1	137000	7929.0	3079.2	7564.7	8107.0	6099.3	4355.4
GQ076185.1	449255	8388.5	7142.7	5132.1	10696.8	9575.6	9346.7
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GQ094377.1	394271	9990.6	5922.5	12817.1	10687.6	6713.5	9072.0
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EU676430.1	302458	5737.3	3755.2	12031.1	9438.5	1490.9	5808.9
GQ249361.1	547824	10339.2	3572.7	8749.9	11772.2	4499.4	5634.7
EU800119.1	341614	8635.9	3764.9	6523.3	9944.2	1567.4	3023.6
EU801154.1	314075	6553.9	4902.7	11854.3	12819.9	2053.2	4668.4
EU735706.1	337175	5067.2	5037.6	6540.1	4700.4	4143.6	4787.2
AF502223.1	59344	7896.8	6837.4	12154.3	10376.6	3621.5	5919.0
EF516428.1	220686	2114.3	1977.9	2148.7	1817.5	2930.8	2299.1
GQ009720.1	499945	3185.8	2069.4	4320.5	4418.8	2765.7	3588.1
DQ178978.1	139068	2159.2	974.2	3299.1	2651.8	923.3	2299.2
DQ432053.1	154227	9919.8	3447.8	11918.5	9942.9	3126.3	3792.6
AY160868.1	95932	8554.5	6580.8	13673.4	11251.1	5041.1	5156.0
AJ420329.1	35360	8780.4	4534.2	13082.0	12228.8	4279.5	6766.2
EU169184.1	247107	4285.0	2603.6	7715.5	8830.1	2177.3	4136.7
DQ257419.1	141979	4955.2	2378.8	9249.5	6450.2	2803.9	4501.9
DQ256486.1	144358	8969.3	5934.8	6533.8	7154.4	4345.5	7036.5
AB269775.1	209527	15289.5	14358.4	12542.9	12823.1	15620.9	12014.7
EF641108.1	279410	3271.2	2560.9	1273.8	4358.7	4450.3	4111.8
FJ214196.1	342494	9265.7	4026.5	11589.9	11035.2	2476.0	6440.8
FJ214173.1	327535	11228.3	7731.5	15276.8	14903.3	3282.9	5078.0
FJ214186.1	315987	9954.6	5937.1	10191.4	12578.8	6581.3	6880.8
AJ543434.1	83899	16673.5	12577.2	11921.5	14439.8	10062.9	11142.5

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FJ214204.1 gg_id:340860 Co-speciation earthworms and their nephridial symbionts nephridia clone Ach5-9
DQ327663.1 gg_id:146840 Verminephrobacter foetidai str. EF01-2
DQ327662.1 gg_id:149224 Verminephrobacter foetidai str. EF01-1
NC_008786.1 gg_id:179440 Verminephrobacter eiseniae str. EF01-2
GQ066930.1 gg_id:374294 Topographical and Temporal Human Skin Microbiome skin back clone nbw730f08c1
FJ605423.1 gg_id:430937 Xenophilus aerolata str. PR-1
NR_025114.1 gg_id:571390 Xenophilus azovorans str. KF46F; DSM 13620
EF079087.1 gg_id:247480 Ideonella sp. str. K5.1
DQ664241.1 gg_id:164847 Ideonella sp. str. IMCC1722
AB476705.1 gg_id:547214 SSU sequences prokaryotes inside emergency Gotthard road tunnel Switzerland sulf
AJ421931.2 gg_id:51718 Germany:Elbe River clone Elb197
EU104142.1 gg_id:336502 Evidence Comamonadaceae determinants settling performance activated sludge clo
EF572731.1 gg_id:231452 Coco's Island site 23 marine clone S23_830
CU466908.1 gg_id:356048 Evry wastewater treatment plant anoxic basin clone
EU340221.1 gg_id:251319 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
NR_025916.1 gg_id:555018 Leptothrix discophora str. SS-1; ATCC 43182
EU130970.1 gg_id:243909 Methylibium sp. BAC115
AM774413.1 gg_id:239835 Rivibacter subsaxonicus str. BF49
EU130974.1 gg_id:236153 Methylibium sp. BAC199
AJ422161.2 gg_id:25579 Germany:Spittelwasser River clone Spb111
EF516772.1 gg_id:225864 grassland soil clone FCPP576
AM697195.1 gg_id:217417 sequencing libraries indoor dust clone BF0001C036
FM209333.1 gg_id:571602 Microbial Negev desert s sand soil clone 1250
AY382153.1 gg_id:136994 enriched nonylphenol ethoxylates activated sludge clone S1B10
AY218641.1 gg_id:81483 penguin droppings sediments clone KD4-64
EU536904.1 gg_id:287179 profile human microbiota antecubital fossa (inner elbow) skin clone nbt223f06
AM777983.1 gg_id:239229 nonsaline . Influence pore-size filters determination structure alkaline groundwater
FM209332.1 gg_id:537782 Microbial Negev desert s sand soil clone 225
EU499698.1 gg_id:274988 Field-based laboratory stable isotope probing surveys identities both aerobic and an
EF515904.1 gg_id:226906 grassland soil clone FCPP759
AY771860.1 gg_id:108580 wastewater treatment pool clone SXAU009
DQ837237.1 gg_id:248403 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_11
AB240506.1 gg_id:142476 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites
FJ893771.1 gg_id:540262 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
AY921694.1 gg_id:114102 farm soil clone AKYH1130
GU208509.1 gg_id:580636 Study on Sediment Dongping Lake sediment clone Shf4-24
AF280853.1 gg_id:24241 bioreactor clone mle1-19
AY218657.1 gg_id:103477 penguin droppings sediments clone KD9-144
EU907887.1 gg_id:309250 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v
EU362134.1 gg_id:305378 and Mesquite Flats Site Death Valley dune sand clone 5
EU491350.1 gg_id:259064 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone

FJ214204.1	340860	9465.4	6222.2	10726.9	11638.8	3150.9	5657.4
DQ327663.1	146840	8362.5	5299.6	5453.3	12571.8	6867.9	7463.1
DQ327662.1	149224	16688.0	14852.2	15101.3	18688.8	16634.7	15618.5
NC_008786.1	179440	9801.7	4286.6	10126.7	11633.1	3033.9	5060.3
GQ066930.1	374294	11351.7	5040.0	9440.5	11015.6	2242.6	5107.2
FJ605423.1	430937	4190.8	1789.3	8434.2	7109.3	1083.0	3074.2
NR_025114.1	571390	11094.4	5360.1	11731.0	11029.4	5815.0	7460.9
EF079087.1	247480	2857.8	2952.0	6938.8	3706.6	1722.7	2390.7
DQ664241.1	164847	4740.9	3401.7	6757.0	5677.9	1990.2	4440.6
AB476705.1	547214	7218.6	5599.7	9612.2	5100.1	6465.6	7105.8
AJ421931.2	51718	9913.7	6594.8	9589.8	9018.8	6838.0	8064.5
EU104142.1	336502	3261.5	4785.8	4733.9	3760.8	2058.8	3402.5
EF572731.1	231452	9451.2	7245.3	14437.4	10915.1	6971.0	9285.5
CU466908.1	356048	12808.1	5854.8	9262.4	11697.2	5485.9	7288.7
EU340221.1	251319	4299.1	3131.3	8123.4	4710.0	3827.5	5219.5
NR_025916.1	555018	5468.1	2372.6	10125.5	9221.6	1660.2	4151.0
EU130970.1	243909	6211.8	5248.7	12734.5	9804.6	5110.3	7367.0
AM774413.1	239835	12582.4	7794.5	21335.6	16294.5	9536.2	7672.7
EU130974.1	236153	5729.4	6707.3	11753.3	5319.1	3511.2	5962.1
AJ422161.2	25579	7557.4	4938.2	14200.4	9706.6	4432.9	5687.3
EF516772.1	225864	8908.7	8255.0	11542.9	8913.6	4220.2	7644.0
AM697195.1	217417	14963.2	11876.0	16575.2	18104.2	8767.7	12475.3
FM209333.1	571602	3167.7	3055.6	3437.1	5185.7	2549.2	2531.0
AY382153.1	136994	5422.9	5311.1	8364.0	5055.8	3404.6	6127.5
AY218641.1	81483	11533.2	11413.0	12538.1	9241.6	12498.3	12223.3
EU536904.1	287179	10420.0	9948.8	7747.2	7460.0	10662.8	10102.0
AM777983.1	239229	3967.1	4442.6	9489.9	5166.8	8034.5	8298.3
FM209332.1	537782	3759.2	5559.0	6128.6	5117.6	2723.3	5363.9
EU499698.1	274988	5845.3	7468.6	7311.8	7761.1	5212.6	6854.2
EF515904.1	226906	6247.9	7779.3	6135.4	5780.2	1765.8	3404.3
AY771860.1	108580	423.8	809.8	504.8	389.2	744.3	585.4
DQ837237.1	248403	11411.8	8725.1	10361.3	13686.9	8421.0	9392.3
AB240506.1	142476	6670.9	5548.8	9679.8	9492.3	3578.8	5336.1
FJ893771.1	540262	5336.9	6878.0	16331.1	9600.2	7227.5	4795.2
AY921694.1	114102	7841.3	9941.0	18113.7	14285.0	9885.2	12110.6
GU208509.1	580636	6023.5	6423.4	12951.3	8145.9	5340.7	5026.5
AF280853.1	24241	13343.5	6469.9	12432.7	14113.2	5298.6	7408.3
AY218657.1	103477	2372.1	3133.4	3708.4	4777.2	4248.8	3916.9
EU907887.1	309250	10758.8	7166.1	9575.3	9675.9	6721.3	9197.9
EU362134.1	305378	3652.0	4073.6	5807.1	4030.7	2663.1	4951.3
EU491350.1	259064	16675.5	14140.6	11055.6	16067.6	16132.7	14161.8

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s__Herbaspirillum seropedicae	14340

EF580947.1 gg_id:279576 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM7
AM412128.1 gg_id:239980 Aquabacterium sp. str. P-130
AY212562.1 gg_id:102602 water 10 m downstream manure clone 110ds10
AM697083.1 gg_id:226216 sequencing libraries indoor dust clone BF0002B033
EF999406.1 gg_id:246240 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn
AY218638.1 gg_id:81258 penguin droppings sediments clone KD4-58
GQ043432.1 gg_id:389491 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw9E
DQ676448.1 gg_id:221331 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
EU283391.1 gg_id:236412 consecutively aerated submerged treating domestic wastewater activated sludge m
AB252909.1 gg_id:164634 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 181
FJ478501.1 gg_id:554081 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU639232.1 gg_id:317724 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
DQ298309.1 gg_id:153016 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
FM872725.1 gg_id:366825 occupant source house floor dust clone FB01B01
EF515947.1 gg_id:223606 grassland soil clone FCPT445
EF522266.1 gg_id:217402 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS04
EU881306.1 gg_id:304030 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
FJ478963.1 gg_id:511130 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ640690.1 gg_id:234716 full-scale EBPR sludge clone Skagenf14
EF516703.1 gg_id:226711 grassland soil clone FCPT716
FJ592525.1 gg_id:547327 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
EF020021.1 gg_id:214611 aspen rhizosphere clone Elev_16S_1414
EF580981.1 gg_id:278694 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1
DQ676337.1 gg_id:226112 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AY856848.1 gg_id:111206 Matsuebacter sp. str. 67
AM990542.1 gg_id:277801 Roseateles depolymerans TD CW2-02
AY281140.1 gg_id:100480 Collimonas fungivorans str. CTO 166
AY281150.1 gg_id:105543 Collimonas fungivorans str. NCCB 100029
AJ496445.1 gg_id:57762 Collimonas fungivorans str. CTE227 = NCCB100027
GU441679.1 gg_id:514468 Collimonas sp. str. Cr9-30
GU213333.1 gg_id:560017 Herminiimonas sp. str. 4-96
AJ238357.1 gg_id:7300 Herbaspirillum frisingense str. 75B
EU399917.1 gg_id:267481 Herbaspirillum frisingense str. CAF263
AJ238358.1 gg_id:7301 Herbaspirillum frisingense str. GSF30
FJ657665.1 gg_id:555967 Herbaspirillum frisingense str. B416
AB094401.1 gg_id:69647 Herbaspirillum chlorophenolicum str. CPW301
EU549858.1 gg_id:302270 Herbaspirillum frisingense str. AU14559
EU399918.1 gg_id:275308 Herbaspirillum frisingense str. CAF265
AB021424.1 gg_id:7295 Herbaspirillum rubrisubalbicans str. ATCC 19308T
AJ238356.1 gg_id:7299 Herbaspirillum rubrisubalbicans str. M4
AY191273.1 gg_id:80182 Herbaspirillum seropedicae str. Z152

EF580947.1	279576	10186.5	10028.5	11147.1	10985.0	4958.8	6864.6
AM412128.1	239980	6011.9	6580.7	9978.2	8386.1	3941.0	5222.8
AY212562.1	102602	6598.5	3834.9	11327.7	5487.7	3340.4	2027.5
AM697083.1	226216	8662.9	6323.8	11261.4	10131.2	2666.1	4618.1
EF999406.1	246240	3222.3	4590.1	4573.9	4614.6	2919.1	5036.7
AY218638.1	81258	5241.5	3903.6	1796.8	4411.9	5246.7	5838.4
GQ043432.1	389491	9689.9	3792.5	13724.2	8865.8	2829.5	5566.7
DQ676448.1	221331	13998.8	11555.6	9617.7	5827.6	8024.5	6465.1
EU283391.1	236412	8467.3	8912.1	15505.4	9881.1	6459.9	7791.2
AB252909.1	164634	8745.2	10111.4	11082.7	8999.0	4689.9	9087.2
FJ478501.1	554081	14727.7	10896.7	14830.1	13090.3	5668.6	11697.8
EU639232.1	317724	6873.7	4890.1	9958.1	7260.6	4139.4	6890.1
DQ298309.1	153016	2270.7	3522.6	7857.2	2957.8	4807.4	6637.0
FM872725.1	366825	6712.4	6081.9	12038.1	9810.6	5261.6	6736.7
EF515947.1	223606	4953.8	2768.0	4951.6	4084.0	1749.1	3634.6
EF522266.1	217402	6320.3	5858.9	8345.6	6683.5	5147.1	6027.1
EU881306.1	304030	9578.6	7475.0	16894.0	11904.7	6543.9	6050.0
FJ478963.1	511130	13768.8	12514.6	18536.9	15981.8	10600.6	12049.7
DQ640690.1	234716	1548.3	2151.9	8111.0	6134.2	1372.4	1619.3
EF516703.1	226711	6026.6	6103.6	11742.1	7202.7	1801.4	5081.8
FJ592525.1	547327	775.0	1629.0	4991.7	1623.2	989.0	3051.0
EF020021.1	214611	1412.8	1697.8	4120.8	1592.0	605.0	775.0
EF580981.1	278694	16700.9	15321.6	17407.7	16923.0	13110.9	13017.2
DQ676337.1	226112	2846.8	4765.1	10755.1	4717.5	3397.6	3434.4
AY856848.1	111206	7974.4	3742.3	15183.2	6998.9	3535.5	5156.5
AM990542.1	277801	6088.9	2740.6	6816.3	7115.2	1555.8	3021.3
AY281140.1	100480	4244.1	3828.0	6489.6	6902.5	5607.2	9018.0
AY281150.1	105543	3905.6	3734.7	6470.3	6321.8	5202.4	7578.9
AJ496445.1	57762	3945.4	2174.3	7160.3	5188.8	1609.8	1801.7
GU441679.1	514468	2418.7	2115.4	3710.9	3933.8	2543.4	3626.7
GU213333.1	560017	2705.5	2979.0	4879.5	5550.2	2140.7	3862.2
AJ238357.1	7300	2163.1	3043.3	7076.1	4336.4	7414.5	6055.5
EU399917.1	267481	2644.6	2834.6	6212.9	4748.6	5789.2	6323.8
AJ238358.1	7301	7970.1	6438.2	11243.3	10354.3	9301.7	11756.8
FJ657665.1	555967	4276.4	4351.7	7355.1	5961.8	5663.7	8941.9
AB094401.1	69647	4645.2	4028.0	8337.1	7518.9	4347.4	7281.8
EU549858.1	302270	4307.8	4233.3	7064.5	5977.2	5664.6	8055.8
EU399918.1	275308	4575.8	4231.4	10363.3	9334.3	5665.8	7963.2
AB021424.1	7295	4051.8	3339.2	5094.5	4876.1	7066.7	6777.2
AJ238356.1	7299	1934.5	2691.2	6215.5	5748.0	2617.8	7318.6
AY191273.1	80182	5861.5	5619.2	8611.8	9261.1	6762.7	9733.9

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria
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s__Herminiimonas fonticola	15660
s__unclassified	14491
s__Janthinobacterium lividum	14526
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s__Janthinobacterium lividum	15337
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AF164062.2 gg_id:7313 Herbaspirillum seropedicae str. BA153
EU549854.1 gg_id:299483 Herbaspirillum seropedicae str. AU14073
AY191274.1 gg_id:80833 Herbaspirillum seropedicae str. ZA95
AY191272.1 gg_id:80181 Herbaspirillum seropedicae str. ZA69
AF361023.1 gg_id:74451 Herbaspirillum sp. str. NAH4
AJ505863.1 gg_id:58574 Herbaspirillum sp. str. PIV-34-1 = DSM 14683
AY043371.1 gg_id:63615 Pseudomonas huttiensis str. AU2210A
GU433469.1 gg_id:528777 Herbaspirillum huttiense str. CCBAU 61429
EU024131.1 gg_id:243525 Herbaspirillum huttiense str. CIP 103296
AJ583172.1 gg_id:94668 radioactive site ground water clone S15B-MN104
AY049039.1 gg_id:47876 Pseudomonas huttiensis str. D
AJ238359.1 gg_id:7302 Herbaspirillum frisingense str. Mb11
AB021366.1 gg_id:7292 Pseudomonas huttiensis str. ATCC 14670T
FJ266340.1 gg_id:534872 Herbaspirillum rubrisubalbicans str. RFNB30
FJ605419.1 gg_id:404943 Herbaspirillum rubrisubalbicans str. PPs-3
NR_028656.1 gg_id:584170 Herbaspirillum putei str. 7-2; IAM 15032
AY191276.2 gg_id:80103 Herbaspirillum seropedicae str. M2
AB512142.1 gg_id:564904 Herminiimonas fonticola str. da Costa S-94 (=CIP 108398 =LMG
AB512141.1 gg_id:546345 Herminiimonas saxobsidens str. NEU 1218 (=DSM 18748 =CCM 7436)
EU133873.1 gg_id:251868 tallgrass prarie soil clone FFCH17907
GU244359.1 gg_id:593835 Janthinobacterium sp. str. Lc10-8
EU847234.1 gg_id:353532 Janthinobacterium sp. str. blxAG
FJ894020.1 gg_id:555629 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
FJ193906.1 gg_id:313175 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EU536428.1 gg_id:285908 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213f12
AF529096.1 gg_id:62419 trichloroethene-contaminated site clone ftl206
EU982453.1 gg_id:341939 Enrichment and detection moderate thermophilic microorganisms vents Lau Basin h
AY792243.1 gg_id:119507 Humic Lake clone CrystalBog5B11
FJ267554.1 gg_id:308624 Massilia sp. str. II_Gauze_W_12_10
DQ228653.1 gg_id:142568 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1
FM209304.1 gg_id:571521 Microbial Negev desert s sand soil clone 2321
AM412135.1 gg_id:241097 Massilia sp. str. P-118
GQ354568.1 gg_id:556334 Naxibacter sp. str. HMD2167
EU221406.1 gg_id:235543 Massilia timonae str. H2P8
GQ015305.1 gg_id:494362 Topographical and Temporal Human Skin Microbiome skin palm clone nbw766g11c1
FM209303.1 gg_id:536558 Microbial Negev desert s sand soil clone 2220
GQ098872.1 gg_id:406246 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558b
AB487721.1 gg_id:539718 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
AY792245.1 gg_id:126195 Humic Lake clone CrystalBog2G3
EU431716.1 gg_id:562896 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
EU244075.1 gg_id:365805 16SrRNA probes river Leine sediment clone sl1354

AF164062.2	7313	4990.6	4621.5	8255.4	8242.4	5883.6	8870.8
EU549854.1	299483	3965.1	3278.5	7181.2	6955.0	4702.8	7093.9
AY191274.1	80833	13692.7	13249.5	10109.7	13483.3	10540.1	13125.3
AY191272.1	80181	873.0	489.0	475.8	2238.4	500.8	584.6
AF361023.1	74451	13195.3	10183.4	9929.8	12950.3	9489.7	9289.1
AJ505863.1	58574	1865.2	1858.9	2856.4	2622.1	1584.4	3260.8
AY043371.1	63615	4169.7	2938.5	5360.6	5278.3	3389.9	6661.9
GU433469.1	528777	3924.9	3107.2	4015.5	5706.6	3499.8	7080.1
EU024131.1	243525	9016.5	6149.9	7876.1	8547.5	6253.4	8909.0
AJ583172.1	94668	2432.0	2584.7	689.3	4096.0	6097.8	5723.1
AY049039.1	47876	9251.0	8815.6	6046.6	7466.8	8964.4	10525.2
AJ238359.1	7302	1125.7	1705.3	5015.0	3357.3	924.1	6699.9
AB021366.1	7292	11293.7	5868.2	6636.2	7807.6	4740.6	7740.9
FJ266340.1	534872	2516.8	2861.7	5654.5	6451.9	5226.7	7653.0
FJ605419.1	404943	4143.9	3273.3	5929.4	6343.9	4404.2	7140.7
NR_028656.1	584170	4793.9	4346.4	5777.5	6154.1	4222.0	7756.7
AY191276.2	80103	5304.8	3549.6	7575.1	8560.5	3528.7	6822.0
AB512142.1	564904	1097.7	1665.1	5157.7	3041.4	2198.7	5243.7
AB512141.1	546345	8274.7	6258.6	11232.1	9189.4	6461.3	7166.7
EU133873.1	251868	722.7	1299.9	4745.3	2133.6	1213.0	5441.8
GU244359.1	593835	1388.6	1391.8	6675.0	3780.0	824.3	5918.0
EU847234.1	353532	1395.1	1228.8	2679.9	2034.0	1023.1	6052.2
FJ894020.1	555629	8950.0	9662.4	12624.9	10500.6	7940.2	9110.3
FJ193906.1	313175	4280.9	2803.4	10066.5	9408.6	6316.2	8002.0
EU536428.1	285908	2488.8	2151.4	7424.0	6352.5	6024.0	10825.8
AF529096.1	62419	287.4	879.9	4595.3	1350.7	1257.8	4804.0
EU982453.1	341939	4618.2	3139.2	8964.9	7632.9	1986.6	5051.7
AY792243.1	119507	7256.9	6250.5	8583.4	7471.0	2493.0	6581.9
FJ267554.1	308624	6207.9	4577.8	7955.4	7786.5	4272.7	5941.2
DQ228653.1	142568	8191.5	6759.2	6833.1	6490.8	5697.7	4328.3
FM209304.1	571521	3368.8	2885.7	7761.6	4633.0	2566.0	7434.1
AM412135.1	241097	71.1	181.3	695.5	278.2	103.2	252.7
GQ354568.1	556334	9359.7	8859.9	9964.6	10808.1	12141.3	10072.9
EU221406.1	235543	7765.6	3541.4	7726.9	8102.3	4726.0	7536.7
GQ015305.1	494362	10300.5	6637.9	17798.9	10309.2	7539.7	9010.5
FM209303.1	536558	809.4	1036.0	4188.4	1582.8	990.3	5372.6
GQ098872.1	406246	5698.8	5987.9	9847.9	8572.9	9750.7	10004.6
AB487721.1	539718	6502.4	2746.9	9608.9	4554.6	2880.4	6507.3
AY792245.1	126195	10301.1	5737.0	6950.6	8517.2	8000.5	6679.2
EU431716.1	562896	9055.9	6410.9	13613.4	12712.6	8563.3	7896.4
EU244075.1	365805	532.7	1125.3	2343.3	1745.1	192.0	1095.9

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s__Oxalobacter formigenes	14432
s__Oxalobacter formigenes	15099

FJ192214.1 gg_id:310968 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU249991.1 gg_id:257841 Massilia sp. str. PmeaMuc24
FJ191812.1 gg_id:323439 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AB488284.1 gg_id:569272 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
EU626407.1 gg_id:279407 Massilia sp. str. biosZ4
EU373360.1 gg_id:270893 Massilia timonae str. HNL19
FJ605429.1 gg_id:456558 Janthinobacterium sp. str. PR-2
FJ191801.1 gg_id:331807 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU365682.1 gg_id:269884 Massilia timonae str. M-10
EU160504.1 gg_id:318413 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
EF682966.1 gg_id:246159 Eastern Mediterranean atmosphere clone F27_2E_FL
GQ021547.1 gg_id:488122 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27
AB487246.1 gg_id:558053 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
FJ375473.1 gg_id:510182 T-RFLP powerful tool rapid assessment cells microbial fuel cell sheet carbon paper an
AB234525.1 gg_id:145411 termite gut homogenate clone MgMjD-103
EU274637.2 gg_id:259460 Massilia timonae str. U2
AY966001.1 gg_id:115346 Sinobacter luteus str. 101
AB487486.1 gg_id:567594 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
EU431713.1 gg_id:540535 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
EF516951.1 gg_id:223889 grassland soil clone FCPU439
AJ871463.1 gg_id:110987 Massilia timonae CP183-9
GU377105.1 gg_id:518781 Janthinobacterium sp. str. sptzw14
AF443584.1 gg_id:88301 semiarid soil clone C-F-25
AM412137.1 gg_id:236550 Massilia sp. str. P-127
AF408326.1 gg_id:34181 Massilia sp. clone KL-11-1-5
AM412141.1 gg_id:235451 Oxalobacter sp. str. P-154
AY512824.1 gg_id:106310 Massilia timonae str. S11
EU554441.1 gg_id:275614 Naxibacter haematophilus str. Ag15
AY679161.1 gg_id:102382 Naxibacter alkalitolerans str. YIM 31775
AB097172.1 gg_id:87579 Janthinobacterium sp. str. J3
EU369116.1 gg_id:551576 Janthinobacterium sp. str. AR12
AY599723.1 gg_id:102086 fungal ascocarp clone Cl-73-TB2-II
EU861944.1 gg_id:344291 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
DQ537532.1 gg_id:164523 manganese oxidation soil clone JH-GY25
AJ582187.1 gg_id:93999 soil near uranium mill tailings clone Gitt-GS-70
AM942544.1 gg_id:517426 Duganella sp. str. dug2 CMI-17
EU431682.1 gg_id:557117 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
EF575562.1 gg_id:234460 Duganella sp. str. BD-a14
GQ339887.1 gg_id:580212 Massilia sp. str. MK02
U49752.1 gg_id:70632 Oxalobacter formigenes str. OXWR wild rat cecum
NR_029188.1 gg_id:571425 Oxalobacter formigenes str. OXB; ATCC 35274

FJ192214.1	310968	11178.8	8170.6	10531.3	14223.8	6497.4	10403.8
EU249991.1	257841	2510.6	1203.7	5027.7	2949.7	1303.1	3423.5
FJ191812.1	323439	14847.2	13118.2	10585.6	16930.8	16554.4	17744.2
AB488284.1	569272	2626.8	3307.7	6050.7	5519.4	3260.0	6367.5
EU626407.1	279407	1122.9	762.8	2548.5	1349.8	1463.3	3011.0
EU373360.1	270893	488.6	338.4	627.8	732.1	765.7	1068.5
FJ605429.1	456558	4263.6	2784.1	9324.1	5696.0	3015.3	6679.0
FJ191801.1	331807	15008.0	14580.6	13216.2	15870.9	17275.1	16788.4
EU365682.1	269884	1381.2	1101.2	4845.6	2191.0	1431.6	3237.6
EU160504.1	318413	1758.9	572.4	2115.9	831.2	328.2	1439.9
EF682966.1	246159	9807.7	7670.5	9222.2	11111.9	11377.6	10768.4
GQ021547.1	488122	6278.5	4415.8	11222.7	6821.5	2876.8	5032.8
AB487246.1	558053	16287.0	15944.4	11367.5	13425.1	15985.1	15235.9
FJ375473.1	510182	13939.8	11424.6	13834.1	12917.1	11855.0	13898.0
AB234525.1	145411	3946.9	2432.7	9063.9	4899.5	3732.3	6566.6
EU274637.2	259460	7113.5	4958.6	9769.7	7702.2	4685.4	4996.1
AY966001.1	115346	8172.2	4606.9	10107.8	11109.5	2920.7	5117.8
AB487486.1	567594	5285.9	3777.0	5507.4	5790.6	1531.9	3570.3
EU431713.1	540535	6580.1	4331.3	13589.9	11023.4	4627.8	4518.2
EF516951.1	223889	387.3	718.2	8424.3	1021.0	722.6	1427.4
AJ871463.1	110987	9336.3	11263.0	9939.7	8179.8	8226.5	6064.4
GU377105.1	518781	1645.0	1631.3	5387.6	3173.7	1552.6	3236.0
AF443584.1	88301	6149.7	4906.3	4327.7	4903.2	1242.8	1625.3
AM412137.1	236550	8696.5	8961.3	5848.1	7290.1	9722.9	9161.0
AF408326.1	34181	5969.8	5591.3	7202.0	10911.6	9011.7	8046.9
AM412141.1	235451	14265.1	8941.9	16005.8	13077.9	11682.4	13509.2
AY512824.1	106310	6231.7	3953.6	7166.7	8398.8	5758.2	6074.0
EU554441.1	275614	7736.3	7291.2	15680.0	9357.2	7340.1	9987.4
AY679161.1	102382	16667.0	17682.8	5815.0	15321.9	15985.6	14193.8
AB097172.1	87579	11072.3	7872.5	8409.9	10224.0	12559.6	9787.1
EU369116.1	551576	6069.8	3144.9	5127.7	6534.9	3747.6	8399.1
AY599723.1	102086	2013.6	1386.1	4187.7	1655.3	962.3	1728.5
EU861944.1	344291	2166.5	1712.3	1829.5	1258.1	1295.3	1343.1
DQ537532.1	164523	43.9	100.1	430.1	117.1	280.6	1000.6
AJ582187.1	93999	14619.0	15169.7	9031.1	14634.3	11563.6	10978.1
AM942544.1	517426	763.5	293.9	1951.7	626.3	1496.7	3543.2
EU431682.1	557117	4627.6	4072.1	4819.4	3841.6	7132.8	6919.0
EF575562.1	234460	3907.3	2828.4	7573.3	4811.0	2137.5	6285.0
GQ339887.1	580212	729.6	665.7	1852.4	786.8	308.3	1623.2
U49752.1	70632	8297.8	6860.6	3777.5	12713.7	10972.1	11291.7
NR_029188.1	571425	15775.0	14857.6	9202.6	18024.8	15525.1	15360.5

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U49750.1 gg_id:7366 Oxalobacter formigenes str. BLISS human feces
U49751.1 gg_id:7367 Oxalobacter formigenes str. SOX-4 freshwater lake sediment
U49749.2 gg_id:7365 Oxalobacter formigenes str. BA4 human feces
U49758.1 gg_id:7372 Oxalobacter formigenes str. HC1 human feces
U49756.1 gg_id:7371 Oxalobacter formigenes str. OXK human feces
FJ264587.1 gg_id:331690 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AB488167.1 gg_id:559492 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
U49754.1 gg_id:7369 Oxalobacter formigenes str. OXCR laboratory rat cecum
AB486719.1 gg_id:591499 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0
FJ374254.1 gg_id:363874 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
EF454731.2 gg_id:217779 termite hindgut clone 290cost002-P3L-2608
EF434363.1 gg_id:216215 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont
AB288876.1 gg_id:202850 termite gut homogenate clone BOf1-03
DQ796767.1 gg_id:174649 human fecal clone RL179_aao54b12
FJ269064.1 gg_id:340557 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil
DQ676429.1 gg_id:224948 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AB038368.1 gg_id:19906 Diaphorina citri symbiont
FJ371291.1 gg_id:360508 feces adult twins and mothers; TS6 clone TS6_a03c02
AB234524.1 gg_id:145512 termite gut homogenate clone MgMjD-092
AF371862.1 gg_id:50320 swine intestine clone p-2518-18B5
X92555.1 gg_id:7343 Paucimonas lemoignei str. LMG 2207 T
AB487570.1 gg_id:592988 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
GQ022806.1 gg_id:486864 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
AY177773.1 gg_id:78721 soil clone
GQ069768.1 gg_id:401837 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw7
DQ248254.1 gg_id:141616 carbon tetrachloride contaminated soil clone UE7
AY509446.2 gg_id:99154 freshwater clone LiUU-5-340
DQ351915.1 gg_id:172665 manganese oxidation soil clone JH-WH04
GU213338.1 gg_id:593816 Janthinobacterium sp. str. 338
AM292626.1 gg_id:173162 Influence uranyl and sodium nitrate on natural soil uranium mining waste pile clone
DQ537535.1 gg_id:162048 manganese oxidation soil clone JH-GY37
AY167838.1 gg_id:101564 Janthinobacterium agaricidamnosum str. SAFR-022
AB240320.1 gg_id:144767 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AB487490.1 gg_id:569658 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
EU801571.1 gg_id:317157 It's all ranking aquatic Chesapeake Bay MD clone 3C002897
AM888196.1 gg_id:247545 Herbaspirillum sp. str. THWCSN35
EF516890.1 gg_id:226310 grassland soil clone FCPU733
DQ906892.1 gg_id:256121 Oman subsurface soil clone 12A-1
AY080915.1 gg_id:61192 acidic forest soil clone UP9
AM991238.1 gg_id:279160 Microbial groundwater and their potential use biomonitoring karst spring water clo
AF468345.1 gg_id:79836 Arctic sea ice ARK10157

U49750.1	7366	5704.6	6736.1	8039.9	9280.7	9076.9	10153.1
U49751.1	7367	2735.4	2487.4	6932.4	5850.9	2713.3	3526.5
U49749.2	7365	9020.2	9805.6	7701.0	10268.9	12818.2	11818.8
U49758.1	7372	13746.8	16329.8	10249.2	14311.3	15839.6	15737.7
U49756.1	7371	13658.5	14542.1	14498.6	14539.6	19364.7	16454.9
FJ264587.1	331690	4127.9	5777.2	9752.8	7689.8	6584.6	10222.0
AB488167.1	559492	7837.9	9432.6	10169.5	7827.0	8073.3	9552.5
U49754.1	7369	2124.2	2627.3	6507.9	4125.5	3694.1	5054.3
AB486719.1	591499	5439.5	2183.2	7434.1	8509.1	2115.0	3019.1
FJ374254.1	363874	4352.7	3855.0	11915.6	7777.5	8547.5	9482.2
EF454731.2	217779	263.0	299.1	541.3	1498.5	142.2	354.5
EF434363.1	216215	3371.7	3898.6	5124.9	5311.5	6067.0	8686.2
AB288876.1	202850	2938.2	3574.0	6112.6	7050.2	1481.9	2367.5
DQ796767.1	174649	5915.4	6600.9	6003.8	9587.3	9621.4	11430.1
FJ269064.1	340557	1933.6	2444.1	4901.7	3895.9	2459.4	4072.6
DQ676429.1	224948	1079.6	1049.9	957.3	1974.7	1144.6	1547.9
AB038368.1	19906	353.0	702.3	795.9	1319.4	1187.3	505.8
FJ371291.1	360508	8943.7	9235.4	9262.6	9479.5	6771.7	7015.8
AB234524.1	145512	4926.5	4262.2	7917.1	10308.5	2110.8	2219.9
AF371862.1	50320	2831.8	2889.2	3126.9	2866.5	1989.8	2374.4
X92555.1	7343	2879.6	2898.7	4155.4	4597.9	1067.5	3226.1
AB487570.1	592988	7256.1	6675.9	10566.1	7605.0	4556.4	9495.9
GQ022806.1	486864	9930.8	9832.4	7180.6	10865.8	10149.3	9760.3
AY177773.1	78721	340.6	593.2	1990.2	1149.9	3834.9	6498.1
GQ069768.1	401837	1595.7	1453.3	3649.2	7133.8	1784.6	3042.8
DQ248254.1	141616	1813.8	1825.7	3404.6	3589.6	3094.4	6974.6
AY509446.2	99154	4318.7	3357.4	2695.5	6037.9	5936.7	5587.0
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AM292626.1	173162	4653.9	4304.0	6085.4	7669.0	3547.7	5212.0
DQ537535.1	162048	2048.2	2037.2	3491.9	2844.2	1702.0	3096.2
AY167838.1	101564	121.1	522.4	1930.7	538.0	246.6	3602.4
AB240320.1	144767	4337.2	2758.5	1696.6	5031.6	4796.4	5185.1
AB487490.1	569658	2004.5	1735.6	5313.8	1949.0	3982.1	4651.2
EU801571.1	317157	7412.9	4861.2	15237.8	10800.8	5599.6	5892.2
AM888196.1	247545	3504.4	2272.4	4796.5	4143.4	891.3	2508.2
EF516890.1	226310	488.1	772.3	5764.8	1896.7	550.4	2993.7
DQ906892.1	256121	6010.7	5942.0	4729.8	2969.7	2303.4	3781.6
AY080915.1	61192	4801.1	2823.1	9541.6	9193.9	5603.6	6042.0
AM991238.1	279160	6592.1	5378.4	8223.9	7022.1	9830.8	8852.4
AF468345.1	79836	10662.7	7762.0	13905.8	13229.6	7719.7	10328.8

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DQ351922.1 gg_id:171844 manganese oxidation soil clone JH-GY15
AM397629.1 gg_id:169981 Undibacterium sp. str. CCUG 49012
EU802136.1 gg_id:335152 It's all ranking aquatic Chesapeake Bay MD clone 3C003549
EF516112.1 gg_id:225949 grassland soil clone FCPT483
FM874576.1 gg_id:357346 occupant source house mattress dust clone MD03G10
DQ351928.1 gg_id:171310 manganese oxidation soil clone JH-GY06
EF516828.1 gg_id:225672 grassland soil clone FCPP661
EF516978.1 gg_id:222289 grassland soil clone FCPU492
EF580950.1 gg_id:278562 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM8!
AY082467.1 gg_id:67839 neutral pH mine biofilm clone 44a-B1-39
FM209308.1 gg_id:566578 Microbial Negev desert s sand soil clone 3303
AM697265.1 gg_id:222537 sequencing libraries indoor dust clone BF0001C106
GU321360.1 gg_id:561332 Massilia sp. str. NMC24
GU295961.1 gg_id:585352 Oxalicibacterium sp. str. JCN-21
AB487226.1 gg_id:562136 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0(
DQ787695.1 gg_id:166885 holocene lake sediment clone SLB419
DQ241394.1 gg_id:144017 simple biogeochemical process removing arsenic mine drainage water clone LOP-89
FM872500.1 gg_id:362441 occupant source house floor dust clone FA01C01
AJ863414.1 gg_id:121741 poplar tree microcosm rhizosphere flooded clone 5RHF33
AB487777.1 gg_id:579702 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
GU377118.1 gg_id:532409 Herbaspirillum sp. str. sptzw31
DQ264588.1 gg_id:142425 universal microarray broader than typical library when sampling subsurface groundv
DQ490985.1 gg_id:157892 Pseudoburkholderia malthae str. CC-AFH3
FM955855.1 gg_id:590236 Massilia sp. str. Asd M1A2
EU735672.1 gg_id:345327 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
EU636042.1 gg_id:279632 Antarctic str. N14
EU362137.1 gg_id:352209 and Mesquite Flats Site Death Valley dune sand clone 8
AY198108.1 gg_id:80296 melt pond on Arctic sea ice floe clone ARKMP92
FJ191604.1 gg_id:340957 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AY367012.1 gg_id:93490 ultramicrobacterium str. Um1
EF682968.1 gg_id:255137 Eastern Mediterranean atmosphere clone F13_2C_FL
AM936250.1 gg_id:567104 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GU124500.2 gg_id:570154 endosymbiotic (Stal) (rice brown planthopper) Endosymbiont Nilaparvata lugens clo
EF552158.1 gg_id:233331 Spirillum sp. str. NOX
AJ556800.1 gg_id:85781 Oxalobacteraceae MWH73
AB486782.1 gg_id:592565 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(
FM253595.1 gg_id:341548 Rock gold mine unusually microbial biofilm clone D06-1
AB488125.1 gg_id:548180 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
GQ098449.1 gg_id:401707 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw559g
GQ461666.1 gg_id:533088 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial Bioremedi:
DQ787709.1 gg_id:163192 holocene lake sediment clone SLB530

DQ351922.1	171844	2707.7	4192.0	3220.7	4026.9	3269.1	5380.2
AM397629.1	169981	2763.4	1115.7	3642.2	4546.5	241.8	884.7
EU802136.1	335152	7202.1	4907.7	9761.5	10043.0	4371.0	9202.7
EF516112.1	225949	4967.5	6342.7	9118.5	6685.7	3959.4	7619.6
FM874576.1	357346	7781.8	7437.4	6344.9	7512.8	8475.1	10054.8
DQ351928.1	171310	3778.2	5608.2	4600.2	6022.8	6533.1	8957.8
EF516828.1	225672	2861.9	2079.3	5073.3	3351.4	5008.2	4273.2
EF516978.1	222289	5962.5	2285.7	3686.3	7681.1	2410.3	4696.7
EF580950.1	278562	2625.5	1700.3	6396.1	4214.8	2237.8	3004.4
AY082467.1	67839	442.1	378.4	367.3	690.6	495.4	655.5
FM209308.1	566578	676.8	1454.5	3200.1	1669.3	1464.3	3521.3
AM697265.1	222537	5378.1	5090.3	5643.5	7730.6	4436.2	6421.4
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GU295961.1	585352	3265.1	3831.4	8726.2	5416.0	4873.9	3464.6
AB487226.1	562136	5836.5	4191.1	6716.5	7724.6	4769.0	5883.6
DQ787695.1	166885	16211.1	14135.7	10509.6	14118.0	17499.3	17473.6
DQ241394.1	144017	10855.9	7194.8	5548.9	12672.0	6901.3	8913.5
FM872500.1	362441	3120.0	3622.8	1544.7	2665.1	4026.0	5723.4
AJ863414.1	121741	1017.8	1529.4	8435.1	3375.8	1287.4	3772.9
AB487777.1	579702	2014.0	1180.2	3761.2	1795.0	847.6	2045.6
GU377118.1	532409	4900.2	4071.2	6252.1	6764.2	5333.8	5057.2
DQ264588.1	142425	4956.0	4769.4	5640.6	7035.0	8353.7	7301.4
DQ490985.1	157892	2887.5	4178.9	5505.7	8527.1	5230.8	8729.4
FM955855.1	590236	35.9	68.5	953.3	103.7	89.0	343.7
EU735672.1	345327	1040.2	2302.7	3974.9	3985.6	876.1	4002.3
EU636042.1	279632	5427.6	2162.3	5278.8	5884.7	1376.0	3984.0
EU362137.1	352209	4820.8	4720.9	9041.4	5829.1	3213.0	3936.1
AY198108.1	80296	3844.2	3353.0	7574.5	6406.9	4956.5	7604.1
FJ191604.1	340957	9860.7	11932.5	11953.7	11666.7	15873.0	14454.2
AY367012.1	93490	2036.7	2437.1	4904.1	4723.1	536.2	3227.8
EF682968.1	255137	6781.2	4256.6	6117.6	10115.5	7529.9	7396.8
AM936250.1	567104	7011.6	4103.1	5438.0	9412.2	5921.6	7005.5
GU124500.2	570154	8233.4	5260.1	7740.8	6015.5	3621.2	4594.6
EF552158.1	233331	7429.8	4701.4	5596.2	7639.9	3683.8	6392.3
AJ556800.1	85781	6345.0	5345.6	13381.6	11090.9	3553.9	6309.2
AB486782.1	592565	1201.0	898.6	1114.7	1834.5	1416.1	4291.8
FM253595.1	341548	8232.4	9086.8	12053.9	12341.5	10294.6	10767.2
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GQ098449.1	401707	1603.6	1769.7	4328.0	3452.4	2203.9	1348.9
GQ461666.1	533088	3444.8	3792.5	4755.6	6477.5	3611.2	4880.2
DQ787709.1	163192	4442.7	2029.5	8688.5	7240.6	1088.4	2799.1

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AJ863334.1 gg_id:126321 poplar tree microcosm rhizosphere unflooded clone 4RHU31
DQ248255.1 gg_id:142344 carbon tetrachloride contaminated soil clone UA6
AF358019.1 gg_id:26437 peat soil microcosm clone LO13.5
DQ469209.1 gg_id:157564 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone
AF529095.1 gg_id:62422 trichloroethene-contaminated site clone FTL205
EF620474.1 gg_id:248260 ultramicrobacterium str. ISSDS-831
NR_028859.1 gg_id:566047 Herbaspirillum lusitanum str. P6-12; LMG 21710
DQ017931.1 gg_id:133568 upland stream clone S-Jos_62
DQ787707.1 gg_id:171969 holocene lake sediment clone SLB523
EU676429.1 gg_id:287560 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
EF592558.1 gg_id:232495 Duganella sp. str. B2
AJ582194.1 gg_id:94238 soil near uranium mill tailings clone Gitt-GS-138
DQ177470.1 gg_id:140398 Janthinobacterium sp. str. Tibet-IIK43
EU528198.1 gg_id:286535 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
DQ341421.1 gg_id:150786 Janthinobacterium sp. str. Antarctic IS09
AB008503.1 gg_id:7288 ultramicrobacterium str. MY14
EF682967.1 gg_id:243222 Eastern Mediterranean atmosphere clone F14_4D_FL
EU669620.1 gg_id:329777 soil clone S22-8
DQ158104.1 gg_id:139019 Use Field-Based Stable Isotope Probing Identify Adapted and Track Carbon F throug
EU636048.1 gg_id:278716 Antarctic str. GAo51
EF019643.1 gg_id:215915 aspen rhizosphere clone Elev_16S_794
EU489741.1 gg_id:277881 Herminiimonas sp. str. UMB49
EU636041.1 gg_id:278413 Antarctic str. GA091
AF407411.1 gg_id:21324 MCB-contaminated groundwater-treating reactor clone RB13C5
AY214204.1 gg_id:81252 benzene-contaminated groundwater clone ZZ15C3
EU057874.1 gg_id:253699 Duganella sp. 5B
AB488131.1 gg_id:589716 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
EF515920.1 gg_id:218687 grassland soil clone FCPT636
AY218774.1 gg_id:81640 penguin droppings sediments clone KD6-99
DQ188985.1 gg_id:140045 Herbaspirillum rhizosphaerae str. UMS-40
FJ391493.1 gg_id:364438 primers targeting Gallionella- neutrophilic oxidizers enrichments and soils iron rich irr
GU205377.1 gg_id:583924 Massilia sp. str. DR-a8
AY214210.1 gg_id:81997 benzene-contaminated groundwater clone ZZ17C9
AF468324.1 gg_id:80693 melt pond on Arctic sea ice floe clone ARKMP-20
AJ867677.1 gg_id:109615 melted red snow water clone RS 8-Bact69
AJ295498.1 gg_id:27239 rape rhizosphere clone wr0040
EU194890.1 gg_id:359091 Duganella sp. str. B41
AM085762.1 gg_id:138928 Herminiimonas aquatilis str. CCUG 36956
GU377114.1 gg_id:525330 Janthinobacterium sp. str. sptzw26
GQ451298.1 gg_id:585579 Fecal Yunnan snub-nosed monkey feces clone J308
AB487141.1 gg_id:588705 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0

AJ863334.1	126321	5910.7	6947.3	5747.6	6265.5	8854.9	7411.0
DQ248255.1	142344	5725.2	5218.3	7096.8	7779.9	5717.0	8815.6
AF358019.1	26437	8083.4	4165.5	5295.2	8174.3	5232.1	6619.1
DQ469209.1	157564	5552.1	3691.5	4866.5	7036.5	4172.9	5731.7
AF529095.1	62422	7228.8	6125.4	7172.0	8885.4	3989.2	7444.9
EF620474.1	248260	7915.5	5772.2	9699.3	10381.8	6244.3	7418.1
NR_028859.1	566047	3451.0	4583.8	5879.5	6752.2	1982.7	4315.2
DQ017931.1	133568	2564.4	2556.1	2733.0	6340.2	4780.6	1889.0
DQ787707.1	171969	8966.0	5310.3	2455.6	8816.5	3972.7	8191.5
EU676429.1	287560	6579.4	5838.5	7189.7	7213.1	6274.7	6812.1
EF592558.1	232495	157.3	308.3	2536.8	570.4	142.9	2056.9
AJ582194.1	94238	3695.4	3331.8	6728.8	6590.5	7133.9	8502.0
DQ177470.1	140398	7986.7	3379.8	4209.2	7990.9	3025.5	4908.8
EU528198.1	286535	604.8	1393.6	8049.4	2119.2	1382.0	2176.1
DQ341421.1	150786	1012.5	1253.6	3230.9	1953.4	936.1	2120.0
AB008503.1	7288	826.1	1550.9	2302.1	1591.0	987.4	2264.2
EF682967.1	243222	8100.8	7866.3	8500.0	6826.8	11278.3	11511.5
EU669620.1	329777	1203.6	1532.6	4011.2	2085.4	622.7	3279.7
DQ158104.1	139019	6717.4	7411.2	7586.3	9695.2	7472.9	8882.2
EU636048.1	278716	12961.2	6335.4	12070.1	12297.9	5616.0	6730.1
EF019643.1	215915	78.2	247.7	751.4	192.0	90.7	1006.4
EU489741.1	277881	823.1	1402.9	2767.6	947.3	527.5	3096.5
EU636041.1	278413	7806.8	4402.6	10624.4	8919.9	2663.4	6675.8
AF407411.1	21324	2356.1	2563.4	3780.8	6066.7	3330.0	7588.2
AY214204.1	81252	2331.1	2193.1	4040.7	4712.1	1171.0	2225.6
EU057874.1	253699	9363.2	8680.4	13698.8	10159.0	6936.2	8959.5
AB488131.1	589716	4705.6	3224.2	7048.6	7193.4	2713.1	7874.2
EF515920.1	218687	2622.1	2559.1	3819.0	4835.6	1957.9	2740.5
AY218774.1	81640	11511.7	4864.1	9033.4	10626.1	5936.2	6615.5
DQ188985.1	140045	6597.4	4693.8	7723.8	5895.6	6747.8	8428.8
FJ391493.1	364438	463.3	765.0	3785.2	1407.2	1262.1	2163.9
GU205377.1	583924	4719.3	3622.7	11974.9	9211.9	5225.3	5849.1
AY214210.1	81997	10361.7	6953.3	6048.1	6895.4	5161.3	7117.0
AF468324.1	80693	7594.5	7600.5	9717.9	11871.9	7832.2	10521.5
AJ867677.1	109615	3087.3	2753.0	10213.7	6191.0	5822.5	6863.6
AJ295498.1	27239	7981.0	7421.8	10152.7	9426.5	7837.8	9529.3
EU194890.1	359091	4553.4	3882.0	8968.5	7440.6	2837.8	4990.1
AM085762.1	138928	695.6	1579.6	1591.8	1898.9	1634.2	3780.2
GU377114.1	525330	3976.4	3678.4	6362.7	2576.1	3424.0	6303.4
GQ451298.1	585579	2865.4	2471.7	7158.4	7209.7	2332.8	5556.0
AB487141.1	588705	5345.1	3671.7	4580.0	10116.1	4513.7	8874.9

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GU213385.1 gg_id:533732 Janthinobacterium sp. str. 161
AJ867670.1 gg_id:111083 melted red snow water clone RS 8-Bact32
AB487627.1 gg_id:544493 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
AB487567.1 gg_id:588968 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
GU213421.1 gg_id:589183 Janthinobacterium sp. str. 286
EU150263.1 gg_id:278184 acidobacteria and soil Niwot Ridge LTER clone Ni_E6P2
AY198109.1 gg_id:79646 melt pond on Arctic sea ice floe clone ARKMP91
EF018240.1 gg_id:207516 aspen rhizosphere clone Amb_16S_591
EF019746.1 gg_id:216361 aspen rhizosphere clone Elev_16S_922
AF468329.1 gg_id:80338 melt pond on Arctic sea ice floe clone ARKMP-56
FJ422391.1 gg_id:358892 Burkholderia sp. str. CYEB-14
AM411937.1 gg_id:251263 Herbaspirillum sp. str. P-64
EU636047.1 gg_id:278100 Antarctic str. GA045
EU636045.1 gg_id:279284 Antarctic str. GA054
EU636039.1 gg_id:279184 Antarctic str. CC9
DQ264563.1 gg_id:141833 universal microarray broader than typical library when sampling subsurface groundv
EF574525.1 gg_id:232833 site S25 near Coco's Island marine clone S25_869
AB487774.1 gg_id:583648 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
AY061962.2 gg_id:202769 Oxalicibacterium flavum str. TA17; NEU98; LMG21571
EU881344.1 gg_id:329302 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
AB488296.1 gg_id:587787 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
DQ787694.1 gg_id:162906 holocene lake sediment clone SLB418
EU160577.1 gg_id:310584 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
AB488003.1 gg_id:580561 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
AM697274.1 gg_id:222450 sequencing libraries indoor dust clone BF0001C115
AB074523.1 gg_id:66301 Aquaspirillum arcticum str. IAM 14963
AJ867657.1 gg_id:110953 melted red snow water clone RS 8-Bact21
AJ532689.1 gg_id:76765 uranium mill tailings clone Gitt-KF-179
GQ080374.1 gg_id:373791 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AB074524.1 gg_id:56608 Aquaspirillum autotrophicum str. IAM 14942
AY792246.1 gg_id:122054 Humic Lake clone CrystalBog5F8
FJ517670.1 gg_id:568152 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e
GU213418.1 gg_id:572788 Janthinobacterium sp. str. 278
AB487887.1 gg_id:587586 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
GU113050.1 gg_id:583060 soil overlying mountain Manasi County Xinjiang soils influenced underground coal m
AY515386.1 gg_id:111167 sediment Lake Tuusulanjarvi isolate str. F39
AM849431.1 gg_id:236633 Seasonality Piburger See clone PIB-20
FJ535228.1 gg_id:572527 Contamination risk vegetables Arcobacter during post-harvest processing water carr
AY227003.1 gg_id:81741 melt pool on Arctic sea ice floe clone ARKMP-94 proteobacterium
EF094990.1 gg_id:194580 Rubrivivax gelatinosus str. L31
CU466884.1 gg_id:313285 Evry wastewater treatment plant anoxic basin clone

GU213385.1	533732	200.4	399.0	2577.2	594.4	189.7	1831.6
AJ867670.1	111083	5532.0	4607.2	10789.0	7318.2	3021.1	5878.0
AB487627.1	544493	1288.9	2282.7	3633.8	2898.5	2028.5	3197.1
AB487567.1	588968	6744.0	3566.5	6578.2	9333.0	3823.8	9385.5
GU213421.1	589183	6046.6	4299.4	6899.6	7293.8	6881.1	9487.5
EU150263.1	278184	3170.8	2768.7	5506.6	3033.3	2912.5	6949.3
AY198109.1	79646	6048.5	4766.2	5562.2	8630.9	7734.4	8361.2
EF018240.1	207516	4874.7	3237.0	2523.2	5742.6	3960.8	5102.8
EF019746.1	216361	15113.0	13121.0	13488.7	14939.1	14265.3	14648.6
AF468329.1	80338	8960.7	5962.4	12857.3	11665.9	8213.7	11058.7
FJ422391.1	358892	1551.7	2719.2	8725.7	3853.4	939.8	4354.8
AM411937.1	251263	11693.5	10015.7	10570.9	14283.6	13891.8	13563.2
EU636047.1	278100	6218.6	4817.2	7309.1	7409.1	2541.0	5495.2
EU636045.1	279284	8612.1	6516.6	7187.7	10527.0	6337.2	6359.9
EU636039.1	279184	4714.2	3058.6	4116.8	7703.4	3528.5	6966.0
DQ264563.1	141833	4066.9	3584.2	4516.4	4670.3	1758.9	4674.4
EF574525.1	232833	3582.2	2529.2	5323.1	5670.4	3106.3	6724.5
AB487774.1	583648	1970.3	2816.4	4447.9	4827.2	1443.0	3871.1
AY061962.2	202769	1771.3	2056.4	2345.9	2979.0	1787.6	1893.1
EU881344.1	329302	3123.9	3170.9	6277.3	7061.5	4878.4	8377.6
AB488296.1	587787	407.0	765.9	1105.9	1929.1	794.9	2048.3
DQ787694.1	162906	1517.0	1709.9	2960.3	2461.9	1411.7	4351.1
EU160577.1	310584	7013.6	4348.6	14519.5	9808.6	5938.0	6249.4
AB488003.1	580561	2117.8	2491.2	4776.4	4158.8	2930.0	4459.6
AM697274.1	222450	638.2	1383.9	4711.0	2575.3	3889.9	7801.6
AB074523.1	66301	2489.1	2179.3	9221.7	6835.8	3113.0	3788.7
AJ867657.1	110953	40.7	78.4	117.9	99.4	55.9	224.9
AJ532689.1	76765	252.9	973.1	1431.6	826.5	817.6	1630.1
GQ080374.1	373791	2046.3	2393.4	5292.6	2101.7	557.9	954.3
AB074524.1	56608	4214.5	5076.6	4954.0	7601.4	1524.2	3822.7
AY792246.1	122054	2074.0	2036.3	1803.6	4707.6	1436.4	3566.9
FJ517670.1	568152	5938.3	5028.4	10956.3	4678.2	4440.4	6483.7
GU213418.1	572788	650.2	902.2	4218.4	1611.5	451.7	2501.0
AB487887.1	587586	8260.3	7282.9	12854.1	9597.7	8907.7	8844.0
GU113050.1	583060	2245.4	3475.2	3408.5	4945.6	2378.1	3166.4
AY515386.1	111167	9826.4	6484.4	11370.6	11197.6	1794.7	4593.0
AM849431.1	236633	10314.2	8619.2	16036.9	12156.7	6922.6	8026.3
FJ535228.1	572527	10634.9	7745.6	9022.9	6841.9	7216.8	9135.6
AY227003.1	81741	6354.1	2685.3	10757.5	5863.4	2963.0	5304.3
EF094990.1	194580	4245.4	2942.5	6923.9	5501.3	3105.8	6295.6
CU466884.1	313285	16123.6	15670.4	14163.6	13203.1	12242.5	12776.8

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FJ484872.1 gg_id:512841 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
GQ396839.1 gg_id:587796 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
CU466928.1 gg_id:325979 Evry wastewater treatment plant anoxic basin clone
GU454909.1 gg_id:528368 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
CU466864.1 gg_id:327001 Evry wastewater treatment plant anoxic basin clone
CU466850.1 gg_id:338411 Evry wastewater treatment plant anoxic basin clone
GQ249369.1 gg_id:553551 Research on biodiversity sludge bioflim Biological Aeration Filter clone B11
GQ302537.1 gg_id:585468 prokaryotic sediment Shawan methods cold spring clone sw-xj209
AB087565.1 gg_id:80525 Sphaerotilus sp. L8
AB087561.1 gg_id:80068 Sphaerotilus sp. L2
Z18534.1 gg_id:7139 Sphaerotilus natans str. 565
AF309815.1 gg_id:73442 synthetic wastewater tmbr15-22 complete clone wastewater
AF177943.1 gg_id:42541 Tepidimonas ignava str. SPS-1037T
EF648100.1 gg_id:255518 dynamics during produced water treatment aerobic activated sludge clone HB116
AY845054.1 gg_id:110733 Tepidimonas sp. str. I1-1
AY594193.1 gg_id:124693 Tepidimonas arfidensis
EU799903.1 gg_id:338160 It's all ranking aquatic Newport Harbour RI clone 1C227573
AY519354.1 gg_id:107473 Thiomonas sp. str. 51
FM992405.1 gg_id:536889 Thiomonas intermedia
AY455808.1 gg_id:103970 Thiomonas perometabolis str. ATCC 23370
DQ146028.1 gg_id:138509 Thiomonas sp. ML1-60
DQ146101.1 gg_id:138673 Thiomonas sp. ML2-48
DQ146068.1 gg_id:139031 Thiomonas sp. ML2-1
AB462557.1 gg_id:321818 Microbial production and energy source hyperthermophilic prokaryotes geothermal
DQ146030.1 gg_id:138725 Thiomonas sp. ML1-62
DQ146119.1 gg_id:138822 Thiomonas sp. ML2-67
DQ146041.1 gg_id:138202 Thiomonas sp. ML1-74
AB308270.1 gg_id:253106 Thiomonas sp. str. RAN4
DQ146097.1 gg_id:138841 Thiomonas sp. ML2-42
DQ146015.1 gg_id:138792 Thiomonas sp. ML1-48
DQ902578.1 gg_id:189483 Thiomonas sp. str. CS2
DQ146103.1 gg_id:138853 Thiomonas sp. ML2-5
AJ549220.1 gg_id:82391 Thiomonas sp. B3
DQ146013.1 gg_id:138541 Thiomonas sp. ML1-46
DQ145996.1 gg_id:138828 Thiomonas sp. ML1-28
DQ145997.1 gg_id:138475 Thiomonas sp. ML1-29
DQ146024.1 gg_id:138425 Thiomonas sp. ML1-57
DQ146130.1 gg_id:138505 Thiomonas sp. ML2-77
DQ146065.1 gg_id:138239 Thiomonas sp. ML1-97
DQ092334.1 gg_id:181396 Thiomonas sp. str. S10

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GQ396839.1	587796	5732.2	4671.0	8620.0	5500.8	2291.9	3062.5
CU466928.1	325979	3721.1	2368.3	4190.9	4616.1	2593.4	4532.7
GU454909.1	528368	2719.4	3776.1	3398.5	2406.8	2797.1	4642.0
CU466864.1	327001	7060.3	6797.2	10699.3	6614.8	6582.7	5742.3
CU466850.1	338411	12007.6	10960.9	8119.4	11562.2	7100.9	10233.4
GQ249369.1	553551	3191.3	4379.3	5949.6	7424.1	4086.2	6832.5
GQ302537.1	585468	1968.1	2565.7	3769.5	2775.6	1774.4	3002.4
AB087565.1	80525	7395.3	7553.3	7433.0	7737.0	5731.8	7348.7
AB087561.1	80068	16707.2	14753.9	11917.0	13116.2	13338.9	13954.6
Z18534.1	7139	3302.2	1610.1	6534.8	5399.0	1906.9	2551.2
AF309815.1	73442	5075.7	3796.9	10697.1	8606.4	3878.7	5178.4
AF177943.1	42541	4625.6	3796.4	6622.6	8366.2	2027.4	4124.3
EF648100.1	255518	5166.1	4170.1	6917.6	8035.9	4365.2	7182.4
AY845054.1	110733	3674.2	3229.7	4430.3	3536.5	1085.6	1440.3
AY594193.1	124693	2755.7	1604.6	3267.7	3526.4	1039.8	3096.9
EU799903.1	338160	3980.4	5943.6	8905.7	3686.3	6653.0	6695.0
AY519354.1	107473	5613.1	5347.6	5660.5	6106.6	3964.2	6535.8
FM992405.1	536889	8143.3	7564.7	7397.8	9857.0	7182.5	8596.6
AY455808.1	103970	6291.4	7592.4	3655.8	3919.9	5035.6	9754.0
DQ146028.1	138509	15588.8	16556.1	10999.2	13219.0	18774.0	21209.8
DQ146101.1	138673	5733.5	5280.9	4412.5	7101.3	7542.1	10621.7
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AB462557.1	321818	7038.3	7506.5	11632.6	8907.3	6019.3	7354.5
DQ146030.1	138725	5037.0	4499.8	6811.7	6193.2	4528.8	9243.3
DQ146119.1	138822	12032.5	7813.0	10363.3	13808.9	8992.8	14609.4
DQ146041.1	138202	11412.4	13047.9	9415.4	10683.0	11227.0	15777.5
AB308270.1	253106	2584.7	4345.2	5077.0	1980.3	3107.7	2884.0
DQ146097.1	138841	5252.7	5438.1	3701.3	5180.1	7103.0	11028.7
DQ146015.1	138792	14070.8	13364.3	7578.1	11980.3	16247.2	20427.6
DQ902578.1	189483	6614.7	6433.1	3303.6	7616.4	8605.6	7312.1
DQ146103.1	138853	12554.2	12952.0	12663.4	11476.7	15744.4	18067.0
AJ549220.1	82391	7378.4	8913.3	6365.0	8518.7	9885.1	10602.3
DQ146013.1	138541	9751.6	11900.5	8066.0	7338.5	12250.4	14197.7
DQ145996.1	138828	19036.3	17297.4	14270.5	15831.3	21912.6	23436.8
DQ145997.1	138475	18151.5	17809.9	17015.0	15209.9	20794.2	24323.7
DQ146024.1	138425	8196.2	7671.5	14417.9	11018.2	10711.7	13487.7
DQ146130.1	138505	13293.2	11217.1	15338.7	14501.8	8288.2	11416.6
DQ146065.1	138239	8125.9	8246.2	7419.5	8480.1	6623.1	9021.0
DQ092334.1	181396	10103.7	9355.2	11473.6	12078.1	10300.1	11717.1

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DQ146051.1 gg_id:139421 Thiomonas sp. ML1-83
DQ146113.1 gg_id:139348 Thiomonas sp. ML2-6
DQ145982.1 gg_id:139243 Thiomonas sp. ML1-12
DQ419962.1 gg_id:153172 Thiomonas sp. DM-Cd5
DQ145994.1 gg_id:138485 Thiomonas sp. ML1-26
DQ146010.1 gg_id:138230 Thiomonas sp. ML1-42
GU233443.1 gg_id:531748 Thiomonas thermosulfata str. 21071 32621
EU937876.1 gg_id:351331 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY050601.1 gg_id:53885 MCB-contaminated groundwater-treating reactor clone GOUTB18
GU208450.1 gg_id:536615 Study on Sediment Dongping Lake sediment clone Fr2-13
EU937989.1 gg_id:307219 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
EF520449.1 gg_id:229543 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-80
GQ388859.1 gg_id:562874 quality deterioration drinking system during serious red water outbreak clone Z238
GQ390167.1 gg_id:574746 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A12
AM167944.1 gg_id:142153 flora waters upstreaming fluids deep igneous rock aquifers mineral spring clone BB4
FJ391492.1 gg_id:367650 primers targeting Gallionella- neutrophilic oxidizers enrichments and soils iron rich irr
AB475012.1 gg_id:540849 sequences located Engiadina Bassa Valley Switzerland iron containing freshwater sou
EU937953.1 gg_id:356589 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
FM204958.1 gg_id:576266 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
GU208476.1 gg_id:592888 Study on Sediment Dongping Lake sediment clone Shc3-16
FJ391502.1 gg_id:361662 primers targeting Gallionella- neutrophilic oxidizers enrichments and soils iron rich irr
GQ263782.1 gg_id:578300 Structure Simulated Level Waste Site simulated level waste site clone WC1_b2
GQ264147.1 gg_id:589210 Structure Simulated Level Waste Site simulated level waste site clone WC3_88
DQ295905.1 gg_id:148836 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e
GQ388776.1 gg_id:576649 quality deterioration drinking system during serious red water outbreak clone Z10
EU937859.1 gg_id:327025 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY922005.1 gg_id:112903 farm soil clone AKYG404
GQ388790.1 gg_id:593879 quality deterioration drinking system during serious red water outbreak clone Z114
AY766002.1 gg_id:108663 streamer acidic iron-rich spa water clone TrefC4
FJ037638.1 gg_id:310147 biofilms growing tropical warm soda spring Grenada West Indies clone 070218-Grena
GQ339144.1 gg_id:528137 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
GQ390162.1 gg_id:540543 oxic-anoxic interface meromictic crater lake Lac Pavin clone Eub62C711
AM167968.1 gg_id:143643 flora waters upstreaming fluids deep igneous rock aquifers mineral spring clone BB2
GQ339173.1 gg_id:520149 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
FM174362.1 gg_id:541762 biotrickling filter treating loads H2S biology tools clone H2SRC133X
GQ402778.1 gg_id:534649 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
EF562088.1 gg_id:241212 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
GQ339166.1 gg_id:520139 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
EU283473.1 gg_id:278266 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A531
GU183583.1 gg_id:551555 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a
DQ676395.1 gg_id:225924 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M

DQ146051.1	139421	989.5	1426.4	3850.7	1654.4	2682.0	4330.6
DQ146113.1	139348	9381.0	7951.4	5081.0	9412.6	13210.6	13019.5
DQ145982.1	139243	8845.9	9947.8	12102.9	10020.2	16712.9	17139.4
DQ419962.1	153172	6133.7	4665.3	4982.3	7901.6	2962.5	4582.3
DQ145994.1	138485	13688.7	14405.7	7738.9	11549.1	14822.7	17974.0
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GU233443.1	531748	10841.4	10150.2	12707.0	10998.5	8911.9	11663.5
EU937876.1	351331	2501.3	2172.1	11743.7	10066.5	1472.1	3867.0
AY050601.1	53885	7248.5	6502.2	15875.7	7469.2	5964.1	5539.9
GU208450.1	536615	1258.2	568.4	7275.5	2620.8	2108.7	1048.3
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EF520449.1	229543	4733.1	4499.0	8839.1	8304.3	7721.8	6440.0
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AB475012.1	540849	3025.7	3090.5	13849.0	8439.9	5766.4	6940.7
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EF589997.2 gg_id:234236 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
EU937884.1 gg_id:325090 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
GQ263781.1 gg_id:541843 Structure Simulated Level Waste Site simulated level waste site clone WC1_b19
DQ676316.1 gg_id:223362 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
GQ264072.1 gg_id:593060 Structure Simulated Level Waste Site simulated level waste site clone WC3_170
FN430666.1 gg_id:540799 and activity autotrophic Fe(II)-oxidizing nitrate-reducing enrichment clone F29F67
EU937881.1 gg_id:336779 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
DQ386264.1 gg_id:196465 Siderooxidans lithoautotrophicus str. ES-1
GQ388881.1 gg_id:579184 quality deterioration drinking system during serious red water outbreak clone Z40
EU937923.1 gg_id:336177 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
GQ389039.1 gg_id:553899 quality deterioration drinking system during serious red water outbreak clone S101
EU937931.1 gg_id:339523 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
DQ640694.1 gg_id:228790 full-scale EBPR sludge clone Skagenf48
EU030485.1 gg_id:242960 microbial beneath sheet west Antarctic ice sheet; KIS sediment clone KIS.B77
AY662039.1 gg_id:137480 uranium-contaminated groundwater clone 015B-E09
AF351237.1 gg_id:16839 obtained coal tar waste-contaminated groundwater clone 8-11
AB176698.1 gg_id:98919 subsurface geothermal water clone HAuD-LB/2-20
DQ386858.1 gg_id:178053 Siderooxidans paludicola str. BrT
AY050584.1 gg_id:21368 MCB-contaminated groundwater-treating reactor clone GOUTA12
GQ389053.1 gg_id:563337 quality deterioration drinking system during serious red water outbreak clone S114
FN430662.1 gg_id:556677 and activity autotrophic Fe(II)-oxidizing nitrate-reducing enrichment clone F25F63
AB252929.1 gg_id:164438 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 472
AB240306.1 gg_id:142150 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
FJ037639.1 gg_id:339910 biofilms growing tropical warm soda spring Grenada West Indies clone 070623-Grena
GU220769.1 gg_id:535045 Microbial mineralization and involved microbial Basin field temperature hydrotherm
GU183582.1 gg_id:573953 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a
AY532538.1 gg_id:104211 uranium-contaminated aquifer clone 1013-1-CG10
GQ389139.1 gg_id:512437 quality deterioration drinking system during serious red water outbreak clone S202
DQ450774.1 gg_id:159803 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EF368015.1 gg_id:214563 Hydrogenophilus halorhabdus str. GI-445
EF368017.1 gg_id:205395 Hydrogenophilus halorhabdus str. 1438
NR_024663.1 gg_id:575778 Hydrogenophilus thermoluteolus str. TH-1; IFO 14978
AY222297.1 gg_id:85885 silica sinter depositing geothermal power station discharge drain clone ST01-SN1D prc
AY820184.1 gg_id:109148 Hydrogenophilus denitrificans str. BDN3
AF402975.1 gg_id:40122 hot spring clone bacteriap16
NC_007404.1 gg_id:138944 Thiobacillus denitrificans str. ATCC 25259
GU208337.1 gg_id:576708 Study on Sediment Dongping Lake sediment clone Se1-13
GQ472408.1 gg_id:555271 Microbial Dongping Lake lake sediment clone 4Db1-18
AM936009.1 gg_id:572819 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB476681.1 gg_id:563379 SSU sequences prokaryotes inside emergency Gotthard road tunnel Switzerland sulf

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DQ676316.1	223362	2104.9	2948.4	18400.0	4863.1	5231.8	3768.6
GQ264072.1	593060	11170.8	7471.6	7351.3	11112.4	7571.4	6006.2
FN430666.1	540799	5602.2	6347.6	14435.3	8288.2	8720.8	5783.9
EU937881.1	336779	9982.9	6185.4	25854.1	12191.4	14878.8	7139.8
DQ386264.1	196465	80.9	121.1	15169.5	3190.5	11046.3	1661.9
GQ388881.1	579184	3317.6	3154.6	8588.4	7782.7	2253.0	4275.0
EU937923.1	336177	8101.4	6762.7	18003.3	11663.0	12200.8	8364.6
GQ389039.1	553899	5300.5	6042.8	11456.1	7503.7	5599.8	6793.3
EU937931.1	339523	3529.0	4324.1	18574.5	8259.5	5119.0	5646.6
DQ640694.1	228790	4737.7	5828.0	8921.1	7086.6	8487.9	10815.1
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AY662039.1	137480	5467.4	3614.6	12745.8	7506.0	13121.1	9853.6
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AB176698.1	98919	341.7	550.3	1111.8	765.8	1178.9	535.2
DQ386858.1	178053	76.8	278.9	437.4	201.1	225.3	456.5
AY050584.1	21368	4867.2	4052.0	10202.3	8869.6	7303.8	5964.3
GQ389053.1	563337	387.8	596.4	7622.7	836.9	4336.9	807.1
FN430662.1	556677	2483.4	2748.3	13523.7	5809.8	2960.5	2079.9
AB252929.1	164438	3174.4	4418.4	13278.7	4963.1	4750.5	3659.3
AB240306.1	142150	418.4	468.8	11503.2	1893.2	4123.9	948.2
FJ037639.1	339910	2433.9	3072.6	11404.8	4664.3	2075.6	3586.9
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AY532538.1	104211	761.8	391.9	3706.2	813.5	255.9	383.7
GQ389139.1	512437	4533.6	3032.7	10189.1	7118.9	7144.3	4397.7
DQ450774.1	159803	1224.8	729.2	7670.5	2335.8	4419.0	815.1
EF368015.1	214563	3157.1	4302.2	3550.4	6795.3	6105.2	6099.8
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NR_024663.1	575778	13909.9	12033.8	14709.8	14138.8	13897.6	11665.5
AY222297.1	85885	4301.1	4947.3	4074.7	5772.2	6232.1	4616.6
AY820184.1	109148	10162.1	7888.3	7813.9	7151.9	5323.0	5673.0
AF402975.1	40122	4443.6	4365.0	4849.9	4491.0	4110.8	3128.9
NC_007404.1	138944	1759.7	1203.6	5515.2	1272.9	1997.1	1498.1
GU208337.1	576708	238.2	438.5	3635.9	1039.3	158.4	283.0
GQ472408.1	555271	3539.3	2919.0	4326.4	3888.2	4432.7	3950.8
AM936009.1	572819	10055.7	11365.4	14072.2	10653.8	13768.5	11008.4
AB476681.1	563379	754.6	2769.4	7023.1	1147.1	249.6	1039.1

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DQ230962.1 gg_id:141755 subsurface water clone DR938CH110701SACH3
FJ167506.1 gg_id:348470 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
EU662520.1 gg_id:589721 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
GQ472333.1 gg_id:542530 Microbial Dongping Lake lake sediment clone 2S4-9
FM213044.1 gg_id:568820 Biodiversity and shifts assessment biology tools Biotrickling treating loads biotricklin
DQ390445.1 gg_id:154067 Thiobacillus sayanicus str. 4HG
DQ676323.1 gg_id:225078 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
DQ499276.1 gg_id:159653 acidic cave snottite biofilm clone CV10
EU735730.1 gg_id:354395 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_G46
EU735731.1 gg_id:351349 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_H29
DQ088733.1 gg_id:133752 subsurface clone BE16FW031601GDW_hole1-31
AY955090.1 gg_id:114460 sediment clone 35-16K
AJ243144.1 gg_id:23915 Thiobacillus denitrificans str. NCIMB 9548
EU735735.1 gg_id:345541 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_K38
AB179662.1 gg_id:104873 groundwater 0.2 m-filterable fraction clone KNA6-NB06
AM934951.1 gg_id:540782 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GU208503.1 gg_id:584889 Study on Sediment Dongping Lake sediment clone Shf3-3
AB179683.1 gg_id:106165 groundwater 0.2 m-captured fraction clone KNA6-EB03
FM213007.1 gg_id:570827 Biodiversity and shifts assessment biology tools Biotrickling treating loads biotricklin
DQ415787.1 gg_id:157109 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
AY133108.1 gg_id:59893 TCE-contaminated site clone ccspost271
GU208385.1 gg_id:583159 Study on Sediment Dongping Lake sediment clone Td2-18
EU676425.1 gg_id:295407 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
GU208247.1 gg_id:549869 Study on Sediment Dongping Lake sediment clone 6S1-11
GU208366.1 gg_id:537091 Study on Sediment Dongping Lake sediment clone Td1-5
AY532567.1 gg_id:101367 uranium-contaminated aquifer clone 1013-28-CG14
DQ228387.1 gg_id:142824 microbial compositions two subglacial possible role microbes chemical weathering p
AB181501.1 gg_id:109267 wastewater biofilm clone SN-84
DQ988290.1 gg_id:180796 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with
FJ982929.1 gg_id:406533 Thiobacillus sp. str. ST22
GU208288.1 gg_id:576433 Study on Sediment Dongping Lake sediment clone Ftb3-6
GQ472327.1 gg_id:571504 Microbial Dongping Lake lake sediment clone 2S3-14
GQ921437.1 gg_id:578101 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w
DQ415784.1 gg_id:158397 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
DQ256331.1 gg_id:141880 subsurface water clone EV818BHEB5102502DRLWq27f055
DQ088746.1 gg_id:129993 subsurface clone BE23FW031301A4RD-12
GQ487949.1 gg_id:593089 Microbial metal soil polluted heavy metals clone T7-107
AJ307935.1 gg_id:18168 derived microbial 'pearl'- community clone sipK89
AM934969.1 gg_id:535954 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB354624.1 gg_id:260306 Laminated iron texture iron-oxidizing calcite travertine iron-rich deposit clone FD015
EF079668.1 gg_id:252105 Thiobacillus sp. K6.2

DQ230962.1	141755	343.6	488.5	432.1	237.6	91.8	120.1
FJ167506.1	348470	1586.0	1577.8	3452.5	2358.4	997.3	719.9
EU662520.1	589721	3891.2	3442.8	12790.0	7964.2	5854.1	7933.1
GQ472333.1	542530	1759.4	1396.8	5155.7	4776.1	2479.7	3419.7
FM213044.1	568820	61.4	280.0	1032.9	82.8	108.6	85.3
DQ390445.1	154067	326.4	362.0	7893.6	3065.2	236.4	258.7
DQ676323.1	225078	7601.3	5171.5	4186.9	10339.0	3496.7	5889.3
DQ499276.1	159653	1239.4	1515.3	8876.9	2024.9	2263.5	1301.2
EU735730.1	354395	3456.4	1394.8	5986.8	4818.3	1538.5	1867.7
EU735731.1	351349	6478.5	5201.1	9556.4	9712.4	7340.6	5874.0
DQ088733.1	133752	163.0	331.3	4467.7	1160.0	220.0	288.7
AY955090.1	114460	315.9	660.7	8777.5	3742.8	231.7	852.6
AJ243144.1	23915	3954.5	5054.3	9021.4	3332.6	4921.1	4098.7
EU735735.1	345541	2696.3	2753.3	9310.1	8463.3	3479.6	5430.3
AB179662.1	104873	2728.3	2777.0	18524.7	9140.6	6165.5	4075.2
AM934951.1	540782	2234.0	4145.3	4814.6	3257.9	6413.0	5626.7
GU208503.1	584889	7776.0	5889.5	13822.0	12089.3	4543.5	6086.1
AB179683.1	106165	1685.9	1599.6	3956.4	3823.9	2676.8	2534.0
FM213007.1	570827	492.6	593.3	2423.9	1732.9	608.9	396.1
DQ415787.1	157109	1917.8	1778.6	12066.2	5884.0	1941.4	2838.0
AY133108.1	59893	1951.1	2913.3	4404.9	2372.5	2064.4	1325.8
GU208385.1	583159	221.0	2161.7	4853.0	1970.1	1891.8	1668.0
EU676425.1	295407	8017.2	7444.9	10773.5	9610.7	11378.0	11593.3
GU208247.1	549869	1817.2	2048.5	7854.9	5148.1	1070.6	2266.3
GU208366.1	537091	483.7	870.0	4556.6	3010.6	610.5	2247.2
AY532567.1	101367	412.8	1519.5	7711.5	3631.7	846.8	1555.9
DQ228387.1	142824	8570.1	8415.9	15566.4	12823.3	12896.6	9385.8
AB181501.1	109267	4277.8	3555.0	8817.1	8760.8	6868.1	5586.6
DQ988290.1	180796	2563.2	2858.8	4170.5	4273.1	2163.6	4034.4
FJ982929.1	406533	3642.9	3564.1	4973.4	6414.5	3633.2	5642.3
GU208288.1	576433	8002.9	7014.3	8990.7	9513.7	10874.3	6856.3
GQ472327.1	571504	12790.5	12555.5	12080.0	11034.9	12422.7	10325.8
GQ921437.1	578101	4494.8	3225.2	7544.4	6885.5	3060.9	4295.8
DQ415784.1	158397	84.3	185.7	238.7	120.4	139.1	81.6
DQ256331.1	141880	1345.7	1211.0	7821.7	5170.1	1190.5	2342.4
DQ088746.1	129993	82.0	220.8	1026.0	158.2	183.2	159.0
GQ487949.1	593089	10543.3	8919.2	11231.6	9445.8	8633.4	7763.6
AJ307935.1	18168	10320.1	8693.0	11657.1	13747.0	8933.0	8156.2
AM934969.1	535954	3244.1	3188.4	6250.1	5032.2	2998.6	2250.5
AB354624.1	260306	1194.5	997.4	5415.8	4636.6	1063.8	550.7
EF079668.1	252105	3326.6	2809.9	8543.1	2351.6	4853.3	3673.0

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AJ295643.1 gg_id:17101 uranium mill tailing clone KF-Gitt2-40
GU208480.1 gg_id:576640 Study on Sediment Dongping Lake sediment clone Shc1-6
AB425057.1 gg_id:274500 sequences / Arvadi Biofilm stones freshwater spring containing (among others) hydr
FJ484024.1 gg_id:537733 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
GU208262.1 gg_id:553029 Study on Sediment Dongping Lake sediment clone 6F2-12
AY510250.1 gg_id:109312 microbial mat sulfidic cave spring Lower Kane Cave clone LKC3_198.8
AB176697.1 gg_id:107729 subsurface geothermal water clone HAuD-LB/2-3
FJ901811.1 gg_id:538289 phreatic limestone sinkholes northeastern Mexico water column surface cenote La Pa
EU037198.1 gg_id:249812 Hot Spring Microbial Mat Khir Ganga India hot spring microbial mat clone MO43
DQ837278.1 gg_id:255039 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_81
AB176695.1 gg_id:107438 subsurface geothermal water clone HAuD-MB/2-1
FJ901837.1 gg_id:558734 phreatic limestone sinkholes northeastern Mexico water column surface cenote La Pa
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DQ145970.1 gg_id:138498 Thiobacillus sp. ML2-16
DQ145974.1 gg_id:138290 Thiobacillus sp. ML2-40
CU924728.1 gg_id:563027 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY510243.1 gg_id:109305 microbial mat sulfidic cave spring Lower Kane Cave clone LKC3_102B.25
DQ145968.1 gg_id:151278 Thiobacillus sp. ML1-72
U58019.1 gg_id:6772 Thiobacillus aquaesulis
AY845252.1 gg_id:110030 Spirillum kriegii str. D-430
FJ901825.1 gg_id:512862 phreatic limestone sinkholes northeastern Mexico water column surface cenote La Pa
FJ484428.1 gg_id:553673 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
DQ145964.1 gg_id:138129 Thiobacillus sp. ML1-16
FJ517027.1 gg_id:569792 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
AJ536815.1 gg_id:110737 magnesite mine clone cMM319-05
DQ837267.1 gg_id:248472 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_30
EF492934.1 gg_id:247725 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EF173352.1 gg_id:186982 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb
AJ316618.1 gg_id:64665 Thiobacillus plumbophilus str. DSM 6690 Gro7
DQ984604.1 gg_id:242053 LY oil-contaminated soil clone LYC068
AM490714.1 gg_id:539260 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
GQ090471.1 gg_id:416305 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
DQ837266.1 gg_id:238477 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_20
GQ388880.1 gg_id:535635 quality deterioration drinking system during serious red water outbreak clone Z4
FJ437813.1 gg_id:559929 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa
DQ837229.1 gg_id:243280 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_49
EU735705.1 gg_id:355524 Biological Arsenic Remediation Project Groundwater Aquifer soil clone 1As11
DQ415761.1 gg_id:157821 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
GU208472.1 gg_id:581588 Study on Sediment Dongping Lake sediment clone Shc5-21
DQ520198.1 gg_id:160396 shal China sequences hypertrophic freshwater lake clone ML-9-101.2

EU685841.1	312879	2389.7	2967.5	15092.8	3585.4	4738.5	3471.5
AJ295643.1	17101	3559.3	2833.9	3376.7	3529.6	3059.8	4040.6
GU208480.1	576640	1918.4	2289.3	9060.5	4583.5	1141.8	1643.9
AB425057.1	274500	3000.0	2234.7	7901.4	2309.4	3882.1	3577.7
FJ484024.1	537733	15046.8	11612.9	10061.4	13413.6	11189.6	11140.3
GU208262.1	553029	7266.7	8391.0	9918.5	8416.0	9795.5	7667.8
AY510250.1	109312	2346.4	849.5	4658.5	3773.1	656.1	1065.6
AB176697.1	107729	720.0	485.2	648.6	279.9	1685.5	353.1
FJ901811.1	538289	2078.4	1342.6	4340.4	3656.9	1494.4	1382.8
EU037198.1	249812	5924.3	5870.9	7670.0	6295.4	9629.9	6718.1
DQ837278.1	255039	1455.9	1913.1	5735.4	4433.4	2913.1	3371.8
AB176695.1	107438	6548.3	8239.8	8452.4	7034.2	8198.7	8094.3
FJ901837.1	558734	8712.4	5092.1	12095.7	11633.1	5936.9	7013.5
AY955086.1	114743	11364.6	10906.6	15050.2	12640.9	8944.4	10120.4
DQ145970.1	138498	208.9	399.4	1394.6	828.0	488.2	887.5
DQ145974.1	138290	1153.9	1190.1	1261.4	2215.7	385.8	1143.2
CU924728.1	563027	332.8	409.0	625.1	600.4	145.7	140.8
AY510243.1	109305	15077.6	17364.2	23402.5	16674.0	17680.4	15429.7
DQ145968.1	151278	2403.9	1713.0	50.2	2626.2	1516.9	2027.8
U58019.1	6772	2491.0	2847.6	2097.0	2772.2	2179.7	1992.2
AY845252.1	110030	152.7	155.4	120.1	132.0	142.7	126.5
FJ901825.1	512862	7847.4	6373.8	9105.9	10343.9	5621.7	6741.0
FJ484428.1	553673	3447.5	3643.6	3525.7	4788.1	2558.5	4717.3
DQ145964.1	138129	11317.2	11883.8	17693.9	5994.6	12093.1	10071.5
FJ517027.1	569792	6314.6	3731.6	8861.1	10173.5	5143.9	5492.6
AJ536815.1	110737	4086.7	2615.4	5232.7	5352.2	2801.9	2698.0
DQ837267.1	248472	5214.8	2855.9	10720.3	6648.5	1856.1	3410.4
EF492934.1	247725	110.0	315.3	4087.0	301.1	273.7	2437.9
EF173352.1	186982	1674.4	1722.6	3749.9	5302.7	1681.3	2936.1
AJ316618.1	64665	716.0	1301.1	3042.5	2776.7	1265.5	2386.8
DQ984604.1	242053	8360.1	5401.4	8787.5	10996.4	8594.4	8116.8
AM490714.1	539260	8640.2	8965.1	3621.3	6931.5	4706.0	6821.3
GQ090471.1	416305	4745.5	4067.1	9025.1	9346.3	9170.9	7278.3
DQ837266.1	238477	7701.5	3798.3	19532.4	8890.5	2524.9	4976.1
GQ388880.1	535635	391.3	819.1	3182.9	300.8	510.8	2433.8
FJ437813.1	559929	3315.2	3026.0	6758.3	7975.5	2897.3	5529.0
DQ837229.1	243280	397.4	732.0	3671.3	707.5	434.9	653.2
EU735705.1	355524	3530.7	1777.9	7417.3	5456.9	2560.7	2830.7
DQ415761.1	157821	5416.4	2991.6	9587.2	7700.9	2011.7	3226.7
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DQ520198.1	160396	3359.2	3557.8	7716.3	5161.9	1543.8	2878.3

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DQ066957.1 gg_id:130688 Lake Washington sediment clone pLW-10
GQ472317.1 gg_id:550530 Microbial Dongping Lake lake sediment clone 2B3-20
EU360497.1 gg_id:269449 pilot biological ferrous iron oxidation mine water treatment plant clone W-Z-54
FJ484433.1 gg_id:551992 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AY532537.1 gg_id:104052 uranium-contaminated aquifer clone 1013-1-CG8
AF407390.1 gg_id:19644 MCB-contaminated groundwater-treating reactor clone Ra9C4
FJ712609.1 gg_id:516574 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
GU208482.1 gg_id:589837 Study on Sediment Dongping Lake sediment clone Shc1-3
AB478665.1 gg_id:543991 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland clo
AY212734.1 gg_id:99462 water 20 m upstream manure clone 3up
EF133508.1 gg_id:175927 Ferribacter polymyxa str. PSTR
AJ519624.1 gg_id:74988 Uranium mill tailings soil sample clone Sh765B-TzT-132 proteobacterium
EU340171.1 gg_id:245116 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
EU676421.1 gg_id:297924 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
EU676422.1 gg_id:290525 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
AJ536818.1 gg_id:109678 magnesite mine clone cMM319-36
AF445741.1 gg_id:41556 travertine hot spring clone SM2G09
NR_025556.1 gg_id:569678 Tepidiphilus margaritifer str. N2-214; DSM 15129
DQ287787.1 gg_id:143113 Methylobacillus flagellatus str. KT
AY298905.2 gg_id:88207 Methylobacillus pratensis str. F31
AY027801.1 gg_id:42693 Aminomonas aminovorus str. C2A1; NCIMB 11268
EU194898.1 gg_id:358307 Methylobacillus sp. str. M8
AY772089.1 gg_id:132690 Methylophilus quaylei str. MT
AB193725.1 gg_id:108436 Methylophilus leisingeri str. DSM 6813
AB193724.1 gg_id:108435 Methylophilus methylotrophus str. NCIMB 10515
DQ287786.1 gg_id:141866 Methylotenera mobila str. JLW8
FM872938.1 gg_id:366699 occupant source house floor dust clone FB04H04
FJ626263.1 gg_id:545204 Microbial larval insect gut field and laboratory sugarcane weevil Sphenophorus (Colec
EU340223.1 gg_id:251118 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
AY436794.1 gg_id:104555 Methylophilus sp. str. ECd5
AY546500.1 gg_id:99740 soda lake sediment clone 1H_31
EF192877.1 gg_id:202563 sediments temperate artificial lake Rapel reservoir sediment clone Rap1_6A
DQ450168.1 gg_id:153929 (Uruguay) Atlantic coastal lagoon clone R7C30
AY948052.1 gg_id:143623 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl
DQ228415.1 gg_id:142498 microbial compositions two subglacial possible role microbes chemical weathering p
FJ444649.1 gg_id:511215 Cotton Rhizosphere cotton rhizosphere clone 2h-19
EU662580.1 gg_id:533328 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
AY947940.1 gg_id:143558 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
EU537789.1 gg_id:285536 profile human microbiota antecubital fossa (inner elbow) skin clone nbt79g11
EU340172.1 gg_id:250544 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
EU801545.1 gg_id:306546 It's all ranking aquatic Chesapeake Bay MD clone 3C002863

DQ066957.1	130688	1386.5	1143.3	6659.5	3680.4	1099.1	1509.4
GQ472317.1	550530	3197.5	2321.4	4972.3	5023.2	2353.6	3334.7
EU360497.1	269449	6572.3	5914.6	11387.2	8669.3	9755.8	8201.2
FJ484433.1	551992	4468.9	4720.8	7411.3	7054.1	5007.7	7005.0
AY532537.1	104052	4679.0	3486.6	11104.5	10007.0	6198.1	4548.0
AF407390.1	19644	5693.1	3116.3	5309.4	7334.5	4831.3	2694.5
FJ712609.1	516574	4716.6	3005.0	7884.1	6544.1	5148.0	7759.0
GU208482.1	589837	8293.8	7789.2	7794.8	12107.2	11487.8	9767.6
AB478665.1	543991	4896.7	4967.1	6491.1	4694.5	2309.9	3297.8
AY212734.1	99462	5110.3	4576.4	4753.1	4393.1	2670.2	4693.5
EF133508.1	175927	935.1	878.4	2311.1	3088.3	1083.8	770.1
AJ519624.1	74988	628.7	660.9	2855.7	1541.8	331.2	795.9
EU340171.1	245116	2041.2	2053.6	8328.6	2891.7	762.7	1113.1
EU676421.1	297924	2887.8	3906.7	4518.0	5832.2	5068.4	7228.6
EU676422.1	290525	3984.1	2125.3	7429.5	4475.1	2081.9	2746.9
AJ536818.1	109678	1972.0	2086.0	3136.9	2824.5	1571.6	1624.0
AF445741.1	41556	93.2	148.3	56.6	118.4	80.4	42.4
NR_025556.1	569678	978.9	301.6	834.8	1954.2	1372.0	2870.5
DQ287787.1	143113	2529.9	2340.3	7564.3	5487.9	3660.5	4402.1
AY298905.2	88207	980.0	585.2	226.7	502.4	516.4	673.1
AY027801.1	42693	6653.8	6316.6	16561.7	12229.3	12560.7	12267.5
EU194898.1	358307	516.0	490.4	1180.0	1440.2	221.2	614.0
AY772089.1	132690	990.7	245.5	2993.2	1877.5	2421.7	2411.4
AB193725.1	108436	8077.3	5974.1	6197.3	5946.7	7903.5	7293.3
AB193724.1	108435	6431.4	6058.2	5489.8	4677.7	5785.3	6653.8
DQ287786.1	141866	235.3	479.5	1699.6	2314.4	452.1	576.3
FM872938.1	366699	10070.1	8827.2	17046.9	15380.6	7415.5	9654.0
FJ626263.1	545204	1476.6	1958.3	11600.1	7333.9	2655.6	3870.2
EU340223.1	251118	2813.4	2453.1	4390.6	6658.6	2843.6	2062.3
AY436794.1	104555	7940.7	7754.7	12432.7	12364.3	13504.0	13175.5
AY546500.1	99740	4626.0	5658.7	12434.8	8966.4	5328.2	3918.8
EF192877.1	202563	6124.0	5759.0	14253.7	10964.7	6991.2	5308.9
DQ450168.1	153929	616.6	1875.9	7051.3	6968.5	858.3	2749.5
AY948052.1	143623	2385.7	4531.9	21456.3	17489.8	2345.9	6099.6
DQ228415.1	142498	3955.3	2967.9	10806.0	9512.0	2849.1	2874.5
FJ444649.1	511215	4536.1	2446.4	8787.3	9577.3	2645.6	3129.8
EU662580.1	533328	505.6	825.1	9549.7	6636.8	1196.9	1914.7
AY947940.1	143558	13837.9	13618.8	15621.3	14381.1	13963.5	13079.1
EU537789.1	285536	4833.9	2808.8	11206.7	8274.5	1713.7	1879.1
EU340172.1	250544	11150.8	8165.8	18147.2	13523.9	11422.8	10159.9
EU801545.1	306546	2830.1	2610.4	14349.9	11332.6	2430.9	3883.3

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DQ378255.1 gg_id:155163 oil-polluted soil clone M38_Pitesti
AY212692.1 gg_id:105727 water 10 m downstream manure clone 244ds10
EF580978.1 gg_id:278346 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1:
EF019146.1 gg_id:206079 aspen rhizosphere clone Amb_16S_1787
EU703371.1 gg_id:396964 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH19
AB464941.2 gg_id:343674 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c
AY486132.1 gg_id:103599 Methylovorus mays str. C
EU268114.1 gg_id:250802 summer Dalian and Liaodong bay determined sea water clone ZL1702
EU799457.1 gg_id:330088 It's all ranking aquatic Newport Harbour RI clone 1C227059
EU287055.1 gg_id:235281 Pacific arctic surface sediment clone B78-91
EU591642.1 gg_id:264560 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic
EU801464.1 gg_id:308817 It's all ranking aquatic Chesapeake Bay MD clone 3C002760
AY238979.1 gg_id:105790 sludge dentrifying reactor fed with methanol clone DSBR-C043
EU804023.1 gg_id:338998 It's all ranking aquatic Lake Gatun clone 5C231706
EU236355.1 gg_id:289508 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91B9
DQ513082.1 gg_id:161213 Microbial life fluids ridge flank crustal fluid clone FS266-46B-03
GQ350653.1 gg_id:543211 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ066956.1 gg_id:135981 Lake Washington sediment clone pLW-13
AJ400352.1 gg_id:29664 marine clone ZD0412
EF492937.1 gg_id:240233 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AY678517.1 gg_id:103273 estuarine sediment clone C319a-R8C-D8
EU801551.1 gg_id:329876 It's all ranking aquatic Chesapeake Bay MD clone 3C002872
AY360530.1 gg_id:137280 Stable isotope probing dynamic methylotroph trophic interactions fungi and protozo
FJ612340.1 gg_id:548303 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.2.8
AY360525.1 gg_id:137243 Stable isotope probing dynamic methylotroph trophic interactions fungi and protozo
GQ340339.1 gg_id:568552 Prokaryotic Marathonas Reservoir Greece water column clone VE08-118-BAC
DQ810320.1 gg_id:170033 Oxygen Minimum Zone Surface- Lower Waters and Other Marine oxygen minimum
AY546509.1 gg_id:101169 soda lake sediment clone 5H_52
EU804036.1 gg_id:306270 It's all ranking aquatic Lake Gatun clone 5C231720
AB294945.1 gg_id:219027 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
EU800826.1 gg_id:328759 It's all ranking aquatic Delaware Bay NJ clone 2C229045
EU037912.1 gg_id:247600 Metabolic Profiles Microbial Chlorinated Pesticides Contaminated Sites Three Geogr
AY360533.1 gg_id:137226 Stable isotope probing dynamic methylotroph trophic interactions fungi and protozo
EU800277.1 gg_id:338875 It's all ranking aquatic Delaware Bay NJ clone 2C228317
GQ350509.1 gg_id:580430 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ472336.1 gg_id:560126 Microbial Dongping Lake lake sediment clone 2S4-17
GU230465.1 gg_id:587327 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
AY792265.1 gg_id:125742 Humic Lake clone CrystalBog021G5
EU287027.1 gg_id:255894 Pacific arctic surface sediment clone B78-63
EF173353.1 gg_id:177340 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb
FJ612406.1 gg_id:584989 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.19

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AY212692.1	105727	4011.8	5638.4	14597.0	8411.6	4886.0	5127.4
EF580978.1	278346	9895.9	6659.5	20138.7	11694.4	9967.8	10388.6
EF019146.1	206079	962.7	1170.2	3964.5	1914.6	491.8	861.5
EU703371.1	396964	2943.7	2109.8	7445.1	8591.0	1494.0	1558.6
AB464941.2	343674	4470.7	6284.8	6446.9	3237.2	9382.5	6687.1
AY486132.1	103599	5571.9	4421.2	13253.0	8894.3	7207.7	9151.7
EU268114.1	250802	4681.8	4640.7	12431.9	13417.1	5844.8	6427.1
EU799457.1	330088	8132.8	9837.3	16214.8	10920.7	11030.6	11622.8
EU287055.1	235281	7100.8	6403.6	16264.8	8714.0	6253.5	3766.3
EU591642.1	264560	9247.8	9818.1	12903.3	13622.3	7737.0	9824.3
EU801464.1	308817	10628.4	12408.2	13217.2	15568.9	8829.0	10358.3
AY238979.1	105790	3133.7	2789.6	13298.8	6986.7	3210.2	3717.2
EU804023.1	338998	11665.0	11024.3	13216.6	14328.5	10485.7	10868.8
EU236355.1	289508	2987.3	2712.9	8543.3	6663.4	1572.3	3641.1
DQ513082.1	161213	12881.2	12646.1	12521.5	14487.7	16482.6	12701.8
GQ350653.1	543211	6118.4	5763.2	11916.3	13395.0	5805.5	6482.8
DQ066956.1	135981	3968.8	3251.1	6183.6	5536.5	3973.8	3447.0
AJ400352.1	29664	7340.8	5589.5	7479.5	12981.5	5691.6	4915.4
EF492937.1	240233	765.4	828.3	1774.3	2091.3	422.1	981.0
AY678517.1	103273	4663.4	4301.9	8469.8	7515.8	4392.9	5964.4
EU801551.1	329876	2987.4	3887.1	4887.1	4713.2	1296.6	1013.8
AY360530.1	137280	5559.0	5673.3	7164.1	6467.0	4750.3	7122.6
FJ612340.1	548303	8144.6	5179.7	6676.7	7473.2	5329.6	6268.5
AY360525.1	137243	4063.7	5328.2	4656.5	5998.5	5851.6	5652.0
GQ340339.1	568552	4017.6	4259.7	15428.1	9980.9	4060.8	4958.6
DQ810320.1	170033	14759.7	14208.0	15245.1	11555.3	11660.8	12735.7
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EU804036.1	306270	7581.0	6028.8	10258.6	13005.3	4665.7	5902.3
AB294945.1	219027	1846.8	1775.2	1146.5	4094.9	1742.6	1376.5
EU800826.1	328759	7311.8	4556.4	5747.4	8479.3	2523.0	3538.6
EU037912.1	247600	3797.7	3038.6	12314.4	6315.3	4129.8	4967.2
AY360533.1	137226	1375.9	2998.4	2640.3	2521.3	6448.2	6238.0
EU800277.1	338875	8116.7	6254.5	18964.2	13798.4	7231.6	5597.0
GQ350509.1	580430	9024.0	10089.1	17238.2	14598.6	14062.5	13819.5
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GU230465.1	587327	12507.8	12164.2	11288.5	11779.8	11646.6	14314.1
AY792265.1	125742	5828.4	4104.0	5274.6	9363.7	5351.1	8494.3
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EF173353.1	177340	4161.4	2840.9	4360.4	8256.5	2249.5	4101.1
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EU803303.1 gg_id:332100 It's all ranking aquatic Lake Gatun clone 5C230853
FJ826390.1 gg_id:567795 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
AJ318162.1 gg_id:24165 Waste-gas biofilter clone BIqi38
EF379433.1 gg_id:212747 sea water Victoria Harbor (Hong Kong) area clone TLC-PA3-8
GU183586.1 gg_id:580735 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a
AJ582036.1 gg_id:93630 soil near uranium mill tailings clone JG36-GS-101
FJ612167.1 gg_id:587500 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.4.51
EU803922.1 gg_id:303542 It's all ranking aquatic Lake Gatun clone 5C231580
EF516180.1 gg_id:222196 grassland soil clone FCPU667
AY360552.1 gg_id:137233 Stable isotope probing dynamic methylotroph trophic interactions fungi and protozo
AF328143.1 gg_id:38266 Simonsiella crassa str. ATCC29447
AF487710.1 gg_id:55486 Alysiella filiformis str. ATCC 15532
EU661705.1 gg_id:282842 Aquitalea magnusonii str. NBRAJG85
EU661703.1 gg_id:284709 Aquitalea magnusonii str. NBRAJG 83
EU661704.1 gg_id:285068 Aquitalea magnusonii str. NBRAJG84
EU741686.1 gg_id:332151 Aquitalea sp. str. LT10-3
GQ916513.1 gg_id:554457 Aquitalea magnusonii str. AOLR15
EU548073.1 gg_id:276722 Aquitalea magnusonii str. 5YN1-11
AB087265.2 gg_id:63985 Neisseria denitrificans str. IAM 14975
AY117557.1 gg_id:63496 Chromobacterium violaceum str. 07
AE016825.1 gg_id:148906 Chromobacterium violaceum str. ATCC 12472
AY117559.1 gg_id:63494 Chromobacterium sp. str. 46
AY117571.1 gg_id:63483 Chromobacterium sp. str. 70
EU372837.1 gg_id:270823 Chromobacterium violaceum str. ESBV 4400
AY117552.1 gg_id:63505 Chromobacterium sp. str. 48
EU693450.1 gg_id:298487 Chromobacterium violaceum str. EAV2
AB426118.1 gg_id:262569 Chromobacterium sp. str. DS-1
AY117565.1 gg_id:63489 Chromobacterium sp. str. 53
AY344056.1 gg_id:101677 Chromobacterium suttsuga str. PRAA4-1
AF328152.1 gg_id:33892 Simonsiella sp. 27381 str. ATCC 27381; ICPB 3601 ATCC
GQ114060.1 gg_id:378482 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
AF328151.1 gg_id:21796 Simonsiella sp. 29465 str. ATCC 29465; ICPB 3648 ATCC
GQ114732.1 gg_id:427571 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
AF328154.1 gg_id:73115 Simonsiella steedae str. ATCC29435
AB087261.2 gg_id:56599 Simonsiella steedae str. IAM 14972
AF328155.1 gg_id:21461 Simonsiella steedae str. ATCC29445
AM397080.1 gg_id:170117 Deefgea rivuli str. WB 3.4-79
FJ347759.1 gg_id:359570 Deefgea sp. str. nsw-4
AB525415.1 gg_id:575021 Eikenella corrodens str. JCM 12952
GQ422740.1 gg_id:574200 Eikenella corrodens str. Moore D25
EF509092.1 gg_id:226450 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru

EU803303.1	332100	8290.8	6083.9	7697.3	10474.3	9422.3	11134.4
FJ826390.1	567795	7523.9	8180.5	10044.4	10152.1	7868.1	8917.3
AJ318162.1	24165	3541.6	3244.7	5915.7	7158.9	2605.8	4255.4
EF379433.1	212747	6825.2	6933.7	14364.4	14318.4	9594.9	9750.2
GU183586.1	580735	4672.5	4009.5	7988.4	5698.2	3645.5	5377.4
AJ582036.1	93630	7164.5	7003.6	4739.2	6417.6	6998.8	6048.9
FJ612167.1	587500	16510.6	15649.2	12086.5	14136.9	15983.3	16430.8
EU803922.1	303542	12513.7	10148.3	13386.9	15327.2	9022.8	13133.9
EF516180.1	222196	3201.2	3750.8	9341.6	9155.5	6171.1	11327.3
AY360552.1	137233	937.9	1269.8	2725.6	2563.5	2174.5	4842.7
AF328143.1	38266	373.7	661.5	8086.9	4451.0	935.0	605.0
AF487710.1	55486	827.8	500.9	2460.8	2158.7	449.2	522.9
EU661705.1	282842	801.8	805.6	2965.4	3231.3	715.2	1523.4
EU661703.1	284709	3198.0	2577.3	2069.6	3813.9	3815.0	4658.0
EU661704.1	285068	5827.3	5091.1	5589.8	7276.1	3538.9	3637.2
EU741686.1	332151	846.6	968.8	4641.4	2157.2	1757.6	3865.7
GQ916513.1	554457	1003.9	1279.8	5874.0	2166.4	597.7	2613.3
EU548073.1	276722	960.0	543.9	2513.0	860.3	1730.6	3655.1
AB087265.2	63985	505.5	434.2	3237.9	617.8	4720.7	1965.8
AY117557.1	63496	445.5	652.0	3760.8	1499.6	1726.5	3308.3
AE016825.1	148906	534.6	984.3	3301.1	2147.5	2636.3	3269.6
AY117559.1	63494	4161.4	4591.5	6186.0	7435.3	5641.7	6245.5
AY117571.1	63483	6693.8	7824.4	12175.5	5284.6	9078.4	8324.1
EU372837.1	270823	2054.4	2128.5	2878.0	3224.1	2718.9	3470.5
AY117552.1	63505	6111.6	5536.6	6293.2	7744.9	7604.7	7874.0
EU693450.1	298487	3816.3	3138.7	4987.2	4879.8	5870.7	6665.3
AB426118.1	262569	3031.9	3177.1	4338.3	4506.4	3648.9	6115.9
AY117565.1	63489	7791.7	6759.9	3857.8	10710.9	8806.9	10256.0
AY344056.1	101677	4816.0	3735.2	5478.5	5717.8	5628.6	6427.6
AF328152.1	33892	3211.5	2436.3	2460.9	2667.8	1666.0	1807.9
GQ114060.1	378482	2458.2	2661.0	3192.5	4053.8	1659.6	3595.3
AF328151.1	21796	284.5	486.3	1173.6	418.8	872.4	1507.3
GQ114732.1	427571	8605.3	7266.9	8468.5	9745.8	10076.0	8522.8
AF328154.1	73115	4661.5	3344.6	2806.1	6784.2	2664.1	5641.4
AB087261.2	56599	4072.9	4352.0	3724.4	4242.5	3084.7	4521.6
AF328155.1	21461	4253.0	2061.8	3909.4	3785.6	1452.2	3981.4
AM397080.1	170117	117.8	146.2	434.4	124.9	129.3	165.1
FJ347759.1	359570	2049.3	2431.2	3809.4	5501.3	1520.3	2852.9
AB525415.1	575021	4878.0	6810.9	7427.8	5893.4	6437.3	6430.8
GQ422740.1	574200	5351.2	4856.6	6746.2	5604.8	4150.2	3938.9
EF509092.1	226450	1250.0	921.9	4989.0	1798.7	2383.8	2563.0

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s__Laribacter hongkongensis	16670
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s__Neisseria bacilliformis	14365
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L06165.1 gg_id:6388 Eikenella species
DQ226069.1 gg_id:141574 Iodobacter sp. Ba725/02
AY628416.1 gg_id:103564 Kingella kingae M04-42
NZ_ACJW02000005.1 gg_id:470523 Kingella oralis str. ATCC 51147
AY644511.1 gg_id:107215 Kingella sp. M03-232
AY349388.1 gg_id:92601 human oral cavity clone JC012
DQ003616.1 gg_id:125235 Kingella genomosp. P1 oral cone MB2_C20
GU227231.1 gg_id:536311 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier
EU118276.2 gg_id:248652 Laribacter hongkongensis str. LHHZ69f
U89333.1 gg_id:6367 Microvirgula aerodenitrificans str. Sgly2
DQ117531.1 gg_id:133808 Neisseria bacilliformis str. MDA1552
AY560519.1 gg_id:98975 Neisseria bacilliformis str. MDA2833
DQ117530.1 gg_id:134552 Neisseria bacilliformis str. CCUG38158
FJ951437.1 gg_id:546099 Neisseria cinerea str. 26035404
AJ239302.1 gg_id:6408 Neisseria elongata str. I3
NZ_ABZQ01000103.1 gg_id:405639 Neisseria gonorrhoeae str. SK-93-1035
AF146369.1 gg_id:6458 Neisseria gonorrhoeae str. 76993
NZ_ABZG01000136.1 gg_id:436675 Neisseria gonorrhoeae str. 35/02
AJ239285.1 gg_id:6466 Neisseria lactamica str. L22
AF398320.1 gg_id:62759 Neisseria meningitidis str. M8237
DQ201326.1 gg_id:139944 Neisseria meningitidis str. CMCC(B)29025
DQ201330.1 gg_id:140124 Neisseria meningitidis str. CMCC(B)29034
AF382302.1 gg_id:65958 Neisseria meningitidis str. M7855
AY146978.1 gg_id:77115 Neisseria meningitidis str. N.451/91
DQ201332.1 gg_id:140512 Neisseria meningitidis str. CMCC(B)29040
DQ201321.1 gg_id:140447 Neisseria meningitidis str. CMCC(B)29204
AF310541.1 gg_id:32179 Neisseria meningitidis str. M239
AF310340.1 gg_id:46099 Neisseria meningitidis str. M7284
AF409943.1 gg_id:60511 Neisseria meningitidis str. M1141
AF310406.1 gg_id:73554 Neisseria meningitidis str. M7153
AF398321.1 gg_id:62758 Neisseria meningitidis str. M8236
AF382305.1 gg_id:70564 Neisseria meningitidis str. M7860
AF382300.1 gg_id:65960 Neisseria meningitidis str. M7891
AF409944.1 gg_id:60507 Neisseria meningitidis str. M2671
GQ294476.1 gg_id:542309 Neisseria meningitidis str. N.381/05
AF398300.1 gg_id:62776 Neisseria meningitidis str. M7745
AF382295.1 gg_id:65965 Neisseria meningitidis str. M7905
AY132143.1 gg_id:59582 Neisseria meningitidis str. M8585
AY132136.1 gg_id:59586 Neisseria meningitidis str. M8579
AY132142.1 gg_id:59580 Neisseria meningitidis str. M8586
AY146975.1 gg_id:76992 Neisseria meningitidis str. N.221/91

L06165.1	6388	692.3	1160.5	1758.9	1030.4	1879.4	1054.6
DQ226069.1	141574	875.3	587.5	2338.9	2025.9	752.3	1535.3
AY628416.1	103564	968.4	1535.6	2765.6	3039.4	1072.2	1782.7
NZ_ACJW02000005.1	470523	2342.8	3193.3	6040.2	4358.9	3165.2	3227.4
AY644511.1	107215	371.9	443.6	1460.3	2189.7	493.1	1142.3
AY349388.1	92601	2667.9	4288.6	6608.6	5150.9	4603.0	5532.5
DQ003616.1	125235	3599.3	3874.0	7108.2	3712.9	3769.8	4170.4
GU227231.1	536311	4237.1	3471.0	4436.7	5390.5	2113.8	3972.1
EU118276.2	248652	108.5	105.8	299.0	310.3	112.2	76.0
U89333.1	6367	1202.1	929.3	1742.1	1722.6	1026.5	1045.1
DQ117531.1	133808	2210.3	2913.0	4333.5	4603.1	5633.4	3503.5
AY560519.1	98975	152.1	267.2	784.7	998.5	1765.4	404.6
DQ117530.1	134552	7923.2	8979.8	4906.9	5706.4	8250.4	6373.5
FJ951437.1	546099	4701.1	3292.2	4983.8	7140.2	4149.5	5457.8
AJ239302.1	6408	5314.6	4757.0	4092.1	6230.3	4342.0	4496.7
NZ_ABZQ01000103.1	405639	3747.9	3590.3	3082.0	2680.2	2877.9	4080.6
AF146369.1	6458	3740.6	3640.3	3546.0	4044.1	3485.0	4910.2
NZ_ABZG01000136.1	436675	3267.1	3600.5	2551.1	2989.9	3069.8	4100.8
AJ239285.1	6466	4117.3	3949.4	6577.1	7292.2	4568.4	5100.2
AF398320.1	62759	1965.0	2298.6	2298.0	4114.7	2593.7	5055.8
DQ201326.1	139944	2200.8	2813.0	1718.4	4906.3	4501.1	5156.9
DQ201330.1	140124	3622.2	3715.8	6280.0	6708.8	5079.2	7462.5
AF382302.1	65958	3186.9	3698.8	4758.2	6006.7	3755.1	5702.1
AY146978.1	77115	1826.3	1866.8	2410.7	3564.3	2348.0	4557.4
DQ201332.1	140512	18873.5	21010.0	13304.8	15400.6	18168.5	18390.1
DQ201321.1	140447	3369.1	5095.4	2574.0	3836.2	3064.0	4472.8
AF310541.1	32179	2146.0	2209.3	3032.7	4629.2	3031.6	5199.7
AF310340.1	46099	2918.3	3367.0	5998.4	5760.8	4991.3	6434.6
AF409943.1	60511	1275.7	1135.5	1493.7	2609.2	1855.9	3380.9
AF310406.1	73554	2020.9	2441.8	2297.4	3900.2	2513.1	5057.7
AF398321.1	62758	2167.8	2561.7	2932.0	4899.5	3238.1	5375.0
AF382305.1	70564	1565.0	2040.1	2139.7	3883.2	2806.0	4293.7
AF382300.1	65960	2037.5	2306.6	2510.2	4177.0	2702.7	5074.5
AF409944.1	60507	2483.1	3349.9	4476.7	5058.7	3667.2	4674.2
GQ294476.1	542309	1528.0	1500.2	1902.3	3538.5	2249.4	4350.4
AF398300.1	62776	2592.7	1746.7	2612.3	3992.0	2525.0	4041.2
AF382295.1	65965	1665.3	1965.7	1882.5	4100.1	2575.7	4787.9
AY132143.1	59582	1470.3	1710.6	1441.5	2945.1	2021.0	3881.2
AY132136.1	59586	2056.7	2344.6	2624.5	3683.7	2151.8	4078.8
AY132142.1	59580	1392.7	1354.3	2269.7	2857.9	1614.7	3249.6
AY146975.1	76992	2088.5	1863.8	2553.8	3797.9	2356.2	4853.3

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AF409946.1 gg_id:60510 Neisseria meningitidis str. M690
AF310540.1 gg_id:18187 Neisseria meningitidis str. M6199
AJ239298.1 gg_id:6444 Neisseria polysaccharea str. P8
AJ239315.1 gg_id:6455 Neisseria polysaccharea str. P7
AJ239308.1 gg_id:6450 Neisseria meningitidis str. HF116
AJ239312.1 gg_id:6471 Neisseria meningitidis str. S3446
AJ239281.1 gg_id:6437 Neisseria pharyngis str. NCTC4590
AJ239282.1 gg_id:6401 Neisseria mucosa str. LNP405
AJ239294.1 gg_id:6443 Neisseria sicca str. Q29
AJ239301.1 gg_id:6447 Neisseria flava str. U40
AF479577.1 gg_id:53760 Neisseria subflava str. NJ9702
EF511930.1 gg_id:217706 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AJ239291.1 gg_id:6429 Neisseria subflava str. U37
FJ823154.1 gg_id:569075 Neisseria mucosa str. TeTa
AF479578.1 gg_id:16823 Neisseria subflava str. NJ9703
L10738.1 gg_id:6396 Neisseria weaveri
AF395911.1 gg_id:51956 Neisseria weaveri VA6362grgr_2001
NZ_ABZO01000111.1 gg_id:440950 Neisseria gonorrhoeae str. PID332
AF398310.1 gg_id:62766 Neisseria meningitidis str. M7724
FJ191618.1 gg_id:354448 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FM874743.1 gg_id:363843 occupant source house dust skin surface swab clone SA02H07
EF511172.1 gg_id:218785 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AF398299.1 gg_id:62778 Neisseria meningitidis str. M7744
AF310565.1 gg_id:32023 Neisseria meningitidis str. M2786
GU233442.1 gg_id:517381 Neisseria iguanae str. NVSL 85737
EF511120.1 gg_id:221884 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
DQ201335.1 gg_id:139970 Neisseria meningitidis str. CMCC(B)29201
AJ239299.1 gg_id:6445 Neisseria cinerea str. F1
FJ192856.1 gg_id:338605 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ191574.1 gg_id:335421 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AY648028.1 gg_id:104161 Neisseria meningitidis str. NZ90/21
AY648033.1 gg_id:99467 Neisseria meningitidis str. NZ00/189
FJ192099.1 gg_id:338921 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AF409940.1 gg_id:60517 Neisseria meningitidis str. M4643
NZ_ACQV01000002.1 gg_id:470738 Neisseria flavescens str. SK114
AF398309.1 gg_id:62767 Neisseria meningitidis str. M7921
EF511128.1 gg_id:221648 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
NZ_ACEN01000027.1 gg_id:470720 Neisseria flavescens str. NRL30031/H210
AY005029.1 gg_id:42684 subgingival dental plaque clone AK105
AF398308.1 gg_id:62770 Neisseria meningitidis str. M7509

GQ294475.1	580789	1687.7	1894.4	1564.7	3445.9	2024.1	4064.9
AF409946.1	60510	1222.3	1111.5	1629.4	2011.6	1324.4	2408.4
AF310540.1	18187	2233.8	2722.6	3056.8	4877.8	3298.2	5396.7
AJ239298.1	6444	4111.7	3409.6	5162.8	7778.7	4081.8	6848.8
AJ239315.1	6455	3233.1	3602.7	3724.6	6744.0	4528.8	6937.0
AJ239308.1	6450	2313.1	1991.1	3183.3	6584.7	3234.6	6523.0
AJ239312.1	6471	3968.7	3890.6	6401.0	8151.9	5820.6	9410.4
AJ239281.1	6437	589.9	389.6	639.7	1097.8	322.5	1007.6
AJ239282.1	6401	4066.3	2994.7	3371.8	4786.7	1897.3	2903.0
AJ239294.1	6443	472.8	268.2	563.2	541.5	146.9	252.5
AJ239301.1	6447	1998.6	1424.1	3260.6	3361.5	1316.0	2607.8
AF479577.1	53760	12431.9	12085.1	9801.7	11747.9	12963.3	11302.0
EF511930.1	217706	333.8	398.2	184.6	909.5	920.6	782.3
AJ239291.1	6429	3381.5	2485.9	3215.4	4041.0	2209.9	3248.9
FJ823154.1	569075	2058.5	1634.3	2196.4	3224.9	1160.9	2626.0
AF479578.1	16823	6426.1	6200.2	8814.8	7012.6	5704.9	4824.2
L10738.1	6396	370.0	230.3	150.9	637.4	223.7	423.2
AF395911.1	51956	1400.6	2177.9	3298.5	4763.4	3029.4	3618.4
NZ_ABZO01000111.1	440950	3528.3	3381.7	2957.7	3177.2	3068.5	4322.0
AF398310.1	62766	2193.8	2782.2	3540.5	5792.1	2606.7	4968.1
FJ191618.1	354448	2570.2	2889.9	4673.7	5049.3	3127.9	4937.5
FM874743.1	363843	3790.5	4027.8	4930.5	6867.6	6241.9	6256.5
EF511172.1	218785	56.3	153.3	55.0	423.1	97.1	93.5
AF398299.1	62778	575.5	842.3	2217.4	2401.5	4018.1	1581.9
AF310565.1	32023	4213.5	4010.2	5187.4	8027.3	4365.8	7084.5
GU233442.1	517381	1116.4	1580.0	3573.9	2004.5	1046.7	1961.1
EF511120.1	221884	6930.9	7713.0	10248.1	7395.8	7790.2	6819.7
DQ201335.1	139970	2695.8	3509.4	4021.6	5482.7	4781.2	6336.6
AJ239299.1	6445	4690.3	3481.2	4620.9	6880.7	3993.8	5453.2
FJ192856.1	338605	5524.1	5885.8	7254.5	6201.5	5349.4	6321.2
FJ191574.1	335421	4422.6	4175.4	6155.2	4618.0	5073.2	5149.7
AY648028.1	104161	2331.5	2122.2	4090.9	4973.3	4081.5	6176.1
AY648033.1	99467	2308.9	1815.3	3024.6	6365.6	2880.1	6251.1
FJ192099.1	338921	3102.9	2638.9	4846.0	2855.1	3824.6	3548.8
AF409940.1	60517	2156.2	1947.1	3066.3	5383.8	2278.6	4993.1
NZ_ACQV01000002.1	470738	3123.0	2108.9	5451.1	2832.2	2244.5	2340.9
AF398309.1	62767	2270.0	2138.5	3534.6	4718.4	3849.3	6580.4
EF511128.1	221648	9259.2	6482.1	7236.2	6362.8	3798.6	6058.0
NZ_ACEN01000027.1	470720	582.5	855.0	598.0	427.3	472.0	603.6
AY005029.1	42684	3057.5	4002.1	5854.1	3914.6	6297.8	4506.4
AF398308.1	62770	2239.7	2456.6	3101.8	6929.2	3493.8	6708.9

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s__Simonsiella muelleri	14731
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s__unclassified	15645
s__unclassified	15857
s__Stenoxybacter acetivorans	14473
s__unclassified	14577
s__unclassified	14706

AY648032.1 gg_id:99318 Neisseria meningitidis str. NZ00/134
DQ201336.1 gg_id:140609 Neisseria meningitidis str. CMCC(B)29202
FJ191449.1 gg_id:316460 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AF382307.1 gg_id:65953 Neisseria meningitidis str. M7925
AF310344.1 gg_id:30575 Neisseria meningitidis str. M3291
EF509732.1 gg_id:218613 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AF310551.1 gg_id:52834 Neisseria meningitidis str. M4797
AF398275.1 gg_id:62802 Neisseria meningitidis str. M812
AF409938.1 gg_id:60518 Neisseria meningitidis str. M4644
FJ191958.1 gg_id:321506 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ201323.1 gg_id:140409 Neisseria meningitidis str. CMCC(B)29019
DQ201329.1 gg_id:140166 Neisseria meningitidis str. CMCC(B)29031
AJ239284.1 gg_id:6465 Neisseria lactamica str. L20
AY132119.1 gg_id:59602 Neisseria meningitidis str. M8574
FJ191979.1 gg_id:350810 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AJ239293.1 gg_id:6442 Neisseria sicca str. Q28
AJ239280.1 gg_id:6428 Neisseria flavescens str. LNP444
FJ192352.1 gg_id:350507 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ976263.1 gg_id:539814 Interindividual healthy human oral microbiota mouth clone 6BBB59
AY132085.1 gg_id:69908 Neisseria meningitidis str. M9097
NZ_ACQV01000025.1 gg_id:470744 Neisseria flavescens str. SK114
FJ192317.1 gg_id:318935 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AF398273.1 gg_id:62803 Neisseria meningitidis str. M1168
AF398301.1 gg_id:62777 Neisseria meningitidis str. M7918
FJ192355.1 gg_id:353666 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ201334.1 gg_id:139856 Neisseria meningitidis str. CMCC(B)29046
AY648034.1 gg_id:99627 Neisseria meningitidis str. NZ00/215
AF398325.1 gg_id:62755 Neisseria meningitidis str. N.33/00
NZ_ACDX01000110.1 gg_id:470729 Neisseria mucosa str. ATCC 25996
L06171.1 gg_id:6402 Neisseria elongata
AF409941.1 gg_id:72478 Neisseria meningitidis str. M1417
AF398252.1 gg_id:62824 Neisseria meningitidis str. M5283
AB194302.1 gg_id:108299 Sivamonas terrae str. KM-45
AF328146.1 gg_id:69998 Simonsiella muelleri str. ATCC29441
FJ976380.1 gg_id:554114 Interindividual healthy human oral microbiota mouth clone 22B524
GQ102572.1 gg_id:447914 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
DQ003630.1 gg_id:126626 human mouth clone MB5_P15
GQ106230.1 gg_id:468425 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw!
EF212919.1 gg_id:214313 Stenoxybacter acetivorans str. TAM-WH4
DQ837616.1 gg_id:164644 structures honeybee intestines and their response insecticidal proteins gut clone HB
AB192065.1 gg_id:144630 termite gut homogenate clone M1NP1-30

AY648032.1	99318	2102.2	1803.9	3126.0	5613.6	2359.2	4991.0
DQ201336.1	140609	9254.0	8733.0	6114.8	10869.4	6353.0	8165.5
FJ191449.1	316460	6964.9	5485.6	7467.0	7331.9	7691.4	7133.9
AF382307.1	65953	2312.7	2350.8	3673.8	6214.0	2794.0	5676.3
AF310344.1	30575	2114.8	2042.7	3513.1	6522.1	3507.7	6191.6
EF509732.1	218613	1133.1	861.3	2326.1	2356.0	3164.7	2788.7
AF310551.1	52834	1421.4	1613.3	1636.9	2660.5	1659.7	2818.3
AF398275.1	62802	2357.7	2615.8	3490.7	6554.0	3135.8	5857.0
AF409938.1	60518	2105.3	2208.8	2991.4	5657.1	2625.2	5205.0
FJ191958.1	321506	4437.9	2876.9	5555.1	4486.5	3761.0	4061.4
DQ201323.1	140409	1746.3	2398.3	3494.5	3074.2	1687.3	3350.4
DQ201329.1	140166	3430.4	3780.6	4394.8	6445.4	4125.7	6922.9
AJ239284.1	6465	5568.5	4825.1	4314.1	9885.9	3878.9	7938.4
AY132119.1	59602	2918.5	3077.8	4317.4	8032.7	4259.4	7605.9
FJ191979.1	350810	1831.7	2306.1	3555.8	3448.5	2748.3	4084.9
AJ239293.1	6442	4694.1	3143.9	4583.3	5884.9	2310.7	3809.4
AJ239280.1	6428	62.4	60.2	94.2	72.2	115.2	87.0
FJ192352.1	350507	1744.6	849.5	1665.0	1732.3	1814.9	2095.7
FJ976263.1	539814	3753.8	3284.2	3966.4	5348.3	3210.1	3301.3
AY132085.1	69908	2443.4	2145.3	2958.2	4662.2	3416.1	5862.3
NZ_ACQV01000025.1	470744	11756.0	11733.8	22581.2	9456.4	11585.7	8620.3
FJ192317.1	318935	2894.7	1660.3	3109.9	3920.3	1996.7	2859.8
AF398273.1	62803	1793.0	1905.1	3072.5	4973.7	2372.0	4397.2
AF398301.1	62777	1752.6	1865.7	2500.5	5766.5	3060.8	5499.3
FJ192355.1	353666	13729.4	13028.3	7779.4	10408.4	8252.7	7730.3
DQ201334.1	139856	3761.5	5050.4	4331.4	5745.4	3221.4	7044.0
AY648034.1	99627	2842.7	2354.3	3324.0	5152.4	3514.5	6442.8
AF398325.1	62755	2507.3	2925.0	3482.3	6549.9	2959.1	6176.7
NZ_ACDX01000110.1	470729	177.8	241.5	684.6	375.9	498.3	239.3
L06171.1	6402	1636.8	2889.0	1284.7	2711.3	2546.5	2616.4
AF409941.1	72478	1949.0	1811.8	3266.3	4728.6	3937.9	6285.0
AF398252.1	62824	1931.8	2148.8	2966.2	5524.1	2617.6	4895.6
AB194302.1	108299	97.4	190.8	388.2	309.8	196.1	232.2
AF328146.1	69998	23.6	31.6	35.9	70.8	55.8	34.9
FJ976380.1	554114	73.9	136.9	711.1	276.2	280.2	87.5
GQ102572.1	447914	1988.2	2584.1	1963.3	1583.6	2256.5	3321.1
DQ003630.1	126626	63.4	174.6	459.8	273.5	277.0	213.1
GQ106230.1	468425	4977.5	8220.2	7865.6	4448.5	7109.2	8553.8
EF212919.1	214313	143.5	119.3	137.4	134.3	82.8	109.1
DQ837616.1	164644	798.3	1109.1	4065.3	972.4	2041.0	2121.5
AB192065.1	144630	493.6	292.4	573.7	795.4	262.5	424.4

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GQ080914.1 gg_id:395260 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081030.1 gg_id:389030 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
EU370420.1 gg_id:264994 Neisseria sp. str. 93S1
GQ081359.1 gg_id:371512 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
AY157705.1 gg_id:75888 Neisseria sp. str. CCUG 46910
GQ068955.1 gg_id:404060 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081249.1 gg_id:397165 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068667.1 gg_id:466523 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
L06166.1 gg_id:6473 Kingella denitrificans
AY721627.1 gg_id:104026 'New Zealand '
GQ081033.1 gg_id:436445 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
FM874017.1 gg_id:359961 occupant source house mattress dust clone MB05B09
FJ356021.1 gg_id:365006 Targeted FACS enrichment groups lab scale systems aerobic lab-scale EBPR activated
FJ502346.1 gg_id:512007 Neisseria sp. str. GRW38
GQ068870.1 gg_id:426828 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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FJ876273.1 gg_id:589124 Neisseria sp. str. CSL 7565
GQ081376.1 gg_id:414774 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068798.1 gg_id:391640 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
FJ356031.1 gg_id:368201 Targeted FACS enrichment groups lab scale systems anaerobic:aerobic lab-scale EBPR
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GQ081072.1 gg_id:384019 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
NR_025742.1 gg_id:558848 Chitinibacter tainanensis str. S1; BCRC 17254
AY426973.1 gg_id:105593 Neisseria canis VA25810gw_03
GQ068787.1 gg_id:376358 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
AJ239288.1 gg_id:6399 Neisseria animalis str. NCTC10212
GQ081076.1 gg_id:449889 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081274.1 gg_id:438498 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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DQ847448.1 gg_id:166045 human forearm skin clone LR2-63
GQ032451.1 gg_id:450185 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ068942.1 gg_id:392219 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ017304.1 gg_id:492364 Topographical and Temporal Human Skin Microbiome skin nare clone nbu119c05c1
GQ081358.1 gg_id:438216 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068691.1 gg_id:466608 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
CU924421.1 gg_id:556357 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
Y17602.1 gg_id:6368 Formivibrio citricus str. DSM 6150

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GQ081030.1	389030	5929.4	7347.3	18475.1	7397.2	11725.0	10677.9
EU370420.1	264994	8742.0	7616.8	9004.0	6229.4	7766.4	4856.4
GQ081359.1	371512	9841.3	11307.6	12304.9	7106.3	11542.8	9781.5
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GQ068955.1	404060	18998.3	19887.4	15187.2	15918.0	22713.9	20352.5
GQ081249.1	397165	6465.0	5950.6	5081.1	7673.5	11603.6	10631.3
GQ068667.1	466523	6102.6	6058.1	8979.2	7718.7	8213.6	8409.0
L06166.1	6473	6334.6	6178.8	8936.7	7164.4	4720.9	6663.3
AY721627.1	104026	1334.8	2192.8	3023.1	1496.4	690.0	1182.7
GQ081033.1	436445	10298.8	12485.5	6740.9	8147.2	7850.2	7093.9
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GQ068870.1	426828	15038.5	16322.5	15204.8	9718.6	13421.2	10444.1
GQ094121.1	457731	1868.1	1968.4	3879.3	4191.5	2248.1	3487.1
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GQ081376.1	414774	8339.5	8224.1	6614.0	9355.8	14264.0	13405.1
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FJ356031.1	368201	6608.0	7323.9	9747.1	7116.5	7241.0	6665.4
DQ836355.1	168478	903.2	966.5	2892.5	3950.4	1247.0	767.2
GQ081072.1	384019	2957.5	3712.0	7591.3	3674.1	5619.8	8113.6
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AY426973.1	105593	2361.9	2014.2	3445.6	4192.4	1677.5	4345.6
GQ068787.1	376358	21874.6	21586.7	11688.5	17380.7	23222.1	19099.1
AJ239288.1	6399	888.9	776.3	1410.5	2567.8	349.6	683.4
GQ081076.1	449889	2209.6	3820.0	6933.9	5120.3	4489.4	6454.5
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GQ068790.1	413125	4825.9	5271.3	14824.0	4851.4	10018.5	10259.9
GQ080929.1	374165	4318.9	5714.7	8346.1	6497.3	7477.7	8127.4
GQ081036.1	418363	6429.7	6817.5	14260.7	4702.6	14441.0	12256.2
GQ068846.1	452848	11977.0	14280.2	5942.5	6923.9	5520.5	9715.2
DQ847448.1	166045	1983.9	1341.2	2135.5	2298.8	2048.4	1787.9
GQ032451.1	450185	6243.9	5507.6	8752.4	9642.1	6165.3	9101.6
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GQ017304.1	492364	17461.0	17475.2	18088.7	16143.3	19074.0	16584.4
GQ081358.1	438216	2583.8	2987.4	6891.6	5872.1	5017.9	7851.1
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FJ470512.1 gg_id:540352 Chinese human cavities healthy oral cavity clone A_D_03_77
GQ131417.1 gg_id:390069 Neisseria sp. oral taxon 014 str. F0314
GQ081262.1 gg_id:401550 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ093550.1 gg_id:374530 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw366b1
GQ068928.1 gg_id:426161 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
FJ236051.1 gg_id:311155 three Parisian treatment plants approaches drinking water clone Joinville2
GQ081304.1 gg_id:418238 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081360.1 gg_id:464829 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081369.1 gg_id:414989 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081000.1 gg_id:459894 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068906.1 gg_id:447199 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068812.1 gg_id:432019 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068905.1 gg_id:467744 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ071854.1 gg_id:435504 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw189b1
GQ041765.1 gg_id:403344 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932c0
AF487709.1 gg_id:58031 Neisseria dentiae str. V33
GQ041790.1 gg_id:437690 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932f05
EU071524.1 gg_id:236675 and resistance microorganisms European clean room ESTEC HYDRA facility clone EHF
GQ041752.1 gg_id:451137 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932b0
GQ081386.1 gg_id:443089 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ080998.1 gg_id:439533 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ081230.1 gg_id:462985 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
FJ593907.1 gg_id:574480 Chitinibacter sp. str. TNR-14
GQ068705.1 gg_id:464085 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
DQ376554.1 gg_id:151309 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin
GQ080988.1 gg_id:456420 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
AJ629192.1 gg_id:129475 Kingella potus str. 3/SID/1128
DQ006842.1 gg_id:118296 Neisseria sp. R-24680
GQ068696.1 gg_id:393940 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ068762.1 gg_id:412554 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ008214.1 gg_id:501454 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ081261.1 gg_id:446559 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
AY005028.1 gg_id:53569 Neisseria sp. oral strain str. B33KA
DQ314581.1 gg_id:148882 chitin-degrading Taiwan C14
AY609199.2 gg_id:140478 Chromobacterium sp. str. 2002
EU536080.1 gg_id:280825 profile human microbiota antecubital fossa (inner elbow) skin clone nbt08d11
AB013258.1 gg_id:6372 deep-sea sediment clone NKB6
AM295491.1 gg_id:164660 Gulbenkianus mobilis str. E4FC31
AY904024.1 gg_id:146009 Aquaspirillum sp. str. 411

EU104028.1	337734	2500.4	3077.6	7621.8	4392.1	4992.6	8431.3
DQ006843.1	115401	2836.3	2104.1	5731.1	5321.8	882.5	2642.0
FJ470512.1	540352	5535.4	5047.0	5350.1	6804.3	4868.7	6356.7
GQ131417.1	390069	3635.2	3583.8	4748.6	5516.2	6022.6	4047.7
GQ081262.1	401550	1774.9	3739.3	6846.1	3828.5	3494.3	3780.5
GQ093550.1	374530	4321.0	4158.2	7556.0	5110.3	6921.7	7930.2
GQ068928.1	426161	7880.4	9254.4	12964.0	6633.5	10216.8	9907.3
FJ236051.1	311155	8122.1	5183.2	14120.5	9422.1	6968.3	6794.4
GQ081304.1	418238	10855.1	12377.4	14428.1	12235.6	14942.5	13885.5
GQ081360.1	464829	24248.4	24345.4	24696.5	19810.2	26228.1	21743.6
GQ081369.1	414989	6545.8	8010.8	13043.2	10115.3	12624.0	10205.4
GQ081000.1	459894	3353.6	4279.0	5834.0	5257.5	7759.1	8175.1
GQ068906.1	447199	3261.4	4026.6	9590.5	7249.3	6919.5	9548.1
GQ068812.1	432019	2183.7	3335.1	6949.4	2144.8	5220.3	5331.4
GQ068905.1	467744	5484.6	7244.0	7034.8	3676.6	4112.4	4063.9
GQ071854.1	435504	18199.2	17371.2	20733.5	16325.8	21483.9	18366.8
GQ041765.1	403344	5511.0	4925.8	6494.5	7471.4	10514.3	11013.9
AF487709.1	58031	1331.4	894.2	2552.4	3344.7	532.3	679.7
GQ041790.1	437690	3112.3	2609.7	7709.6	4749.9	2810.1	4267.1
EU071524.1	236675	5027.9	5500.2	4895.6	3267.2	2946.9	5570.5
GQ041752.1	451137	6037.5	7742.9	5511.0	4993.9	7321.5	8090.1
GQ081386.1	443089	9803.8	11190.5	13004.5	10737.3	11598.0	12191.6
GQ080998.1	439533	2134.8	2639.7	7722.9	4362.2	5319.9	6367.3
GQ081230.1	462985	6299.4	6857.6	6007.8	6070.3	9824.9	8281.4
FJ593907.1	574480	646.6	946.4	1785.6	2030.1	1562.8	2265.5
GQ068705.1	464085	16817.1	15165.7	22819.4	14692.0	14392.1	13707.2
DQ376554.1	151309	8764.7	9204.4	15507.0	12072.0	9262.4	5904.0
GQ080988.1	456420	5223.8	5275.1	10530.3	7218.1	4710.7	7885.0
AJ629192.1	129475	4242.7	3951.4	3943.5	4296.0	2219.9	3407.6
DQ006842.1	118296	3396.6	2422.0	4747.2	4162.2	2557.5	2974.1
GQ068696.1	393940	7291.1	7729.1	10174.4	7227.7	10330.7	12121.4
GQ068762.1	412554	6589.4	9892.0	11409.6	9486.1	16503.5	15517.7
GQ008214.1	501454	2383.8	2111.3	2335.4	4936.5	1846.1	3151.9
GQ081261.1	446559	4650.3	4768.8	5518.2	6011.6	6569.8	7285.9
AY005028.1	53569	666.3	1289.7	957.0	523.3	1753.3	1172.3
DQ314581.1	148882	2557.0	2564.4	1976.8	3504.7	4664.6	3066.9
AY609199.2	140478	2478.1	1675.7	5394.9	4114.5	1508.4	2711.4
EU536080.1	280825	4887.9	4002.3	8163.2	7117.7	5350.1	5385.1
AB013258.1	6372	38.3	45.8	330.5	76.4	46.6	25.4
AM295491.1	164660	1703.7	1601.3	2386.9	3391.6	1561.8	2368.0
AY904024.1	146009	21.0	48.4	73.3	52.1	78.7	25.1

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AB286476.1 gg_id:206343 Reducing production and domination comamonadaceae reducing oxygen supply was
AB076000.1 gg_id:64884 Aquaspirillum putridiconchylium str. IAM 14964
FJ375419.1 gg_id:589312 T-RFLP powerful tool rapid assessment cells microbial fuel cell sheet carbon cloth ano
L06174.1 gg_id:6375 Vitreoscilla stercoraria
AF227863.1 gg_id:36932 str. 82348
AM689950.1 gg_id:226696 Vogesella sp. str. SK-2
AF287297.1 gg_id:29792 Nitrosococcus mobilis str. Nc2
NZ_AAJE01000012.1 gg_id:137518 Nitrosomonas eutropha str. C71
AF272421.1 gg_id:38503 Nitrosomonas sp. NM 41
AJ621028.1 gg_id:105866 Nitrosomonas sp. Is86
AF272413.1 gg_id:40104 Nitrosomonas halophila
FJ529930.1 gg_id:542891 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu
AJ621032.1 gg_id:101077 Nitrosomonas sp. Is343
AF363289.1 gg_id:40156 Nitrosomonas sp. str. K1
EF092247.1 gg_id:265873 Persistent Axinella corrugata Nitrosomonas clone B276_F5
AF272418.1 gg_id:16711 Nitrosomonas marina
AF353164.1 gg_id:22792 Nitrosomonas sp. DYS323
AY123794.1 gg_id:69852 Nitrosomonas sp. str. Nm143
GQ396862.1 gg_id:559849 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EF016119.1 gg_id:182102 Nitrosomonas oligotropha str. AS1
EF092216.1 gg_id:268524 Persistent Axinella corrugata Nitrosomonas clone B2505_H7
GU183580.1 gg_id:583485 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a
AY123795.1 gg_id:69328 Nitrosomonas eutropha str. Nm57
AY123807.1 gg_id:70906 Nitrosospira multiformis str. Nl13; C-71; ATCC 25196
AY856377.1 gg_id:110754 Nitrosospira sp. str. TCH711
AY856375.1 gg_id:109672 Nitrosospira sp. str. HBN8222A
AF353156.1 gg_id:20624 Nitrosospira sp. TCH716
AY123804.1 gg_id:72266 Nitrosospira sp. str. Nsp17
M96404.1 gg_id:6589 Nitrosovibrio tenuis
X84662.1 gg_id:6504 Nitrosospira sp.
AY123803.1 gg_id:69463 Nitrosovibrio tenuis str. Nv1
M96405.1 gg_id:6602 Nitrosovibrio tenuis str. Nv12
AY123800.1 gg_id:70700 Nitrosospira briensis str. Nsp10
AY631269.1 gg_id:102482 Nitrosovibrio sp. FJI82
EU050920.1 gg_id:250427 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_05
AF414581.1 gg_id:33825 uranium mine sediment clone P3OB-51
AF080256.1 gg_id:6535 Nitrosospira sp. str. TYM9
AJ630749.1 gg_id:105991 marine surface water clone BET_1D11G67
EU734961.1 gg_id:311415 assemblages sediment station DBSE Northern Bering Sea clone 054D10
AY123813.1 gg_id:73969 Nitrosospira sp. str. Nsp65
L35505.1 gg_id:6517 Nitrosospira briensis str. C-128

AB286476.1	206343	2015.9	1785.4	2615.0	4654.8	2158.6	3232.7
AB076000.1	64884	38.6	38.0	93.1	86.0	66.9	36.4
FJ375419.1	589312	674.7	1200.9	2524.1	2473.1	912.7	1676.4
L06174.1	6375	7207.6	4681.1	8833.5	11346.1	5006.4	7269.3
AF227863.1	36932	4770.4	3277.4	9562.7	10285.4	3054.0	6373.2
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AF287297.1	29792	125.7	285.4	486.0	237.5	271.6	666.0
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AF272421.1	38503	5630.1	5352.0	7264.4	8693.8	5238.4	5922.6
AJ621028.1	105866	1719.1	2085.5	5569.2	3170.7	2658.0	6924.4
AF272413.1	40104	2191.2	3121.4	4445.0	6431.7	2358.7	4052.5
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AJ621032.1	101077	5324.1	5395.9	13203.7	7793.0	6435.9	7514.1
AF363289.1	40156	379.0	522.1	1743.2	2078.2	460.4	753.6
EF092247.1	265873	7631.3	4999.7	12044.9	10931.5	6252.9	6325.8
AF272418.1	16711	8417.8	10791.3	8454.7	8567.0	9934.2	9684.9
AF353164.1	22792	3482.7	3064.4	9720.9	6853.8	4021.1	4819.6
AY123794.1	69852	1574.2	2068.4	8257.3	4591.1	3560.7	3654.4
GQ396862.1	559849	1069.0	1776.7	3735.2	2357.3	1068.0	5217.3
EF016119.1	182102	1205.4	1583.2	2542.3	2640.4	4054.7	2944.3
EF092216.1	268524	6066.6	6464.5	9936.8	5300.9	8819.7	6703.0
GU183580.1	583485	2927.3	2475.9	5114.1	5940.5	2645.3	5932.4
AY123795.1	69328	2123.1	2030.3	3676.6	3194.6	2090.0	2890.0
AY123807.1	70906	11060.9	11561.5	7012.1	7288.1	9912.4	10395.3
AY856377.1	110754	10186.1	10323.0	7101.0	9678.6	9555.7	8145.1
AY856375.1	109672	6926.7	10053.1	4342.6	3659.0	8413.6	6524.2
AF353156.1	20624	4023.2	4334.4	3027.2	6326.1	5054.8	5511.2
AY123804.1	72266	5339.2	10551.2	4453.6	5477.5	6890.1	6672.8
M96404.1	6589	529.4	619.3	2119.6	1307.6	679.2	423.5
X84662.1	6504	4145.4	5033.9	3817.1	3176.2	3569.0	5294.8
AY123803.1	69463	3162.5	3078.8	9648.9	6241.3	3912.0	4795.6
M96405.1	6602	2859.0	3435.1	12320.8	3929.4	4807.1	4447.0
AY123800.1	70700	4869.4	5550.9	10196.0	6561.0	5794.4	6346.2
AY631269.1	102482	4470.6	5170.5	4265.8	5650.4	5540.0	4251.9
EU050920.1	250427	4916.6	3857.1	7579.8	8976.0	5483.0	5532.2
AF414581.1	33825	4066.2	3878.1	10126.7	7722.4	5262.6	5631.5
AF080256.1	6535	5000.2	3453.0	8434.9	5963.0	4125.1	5406.0
AJ630749.1	105991	4407.7	3786.0	11575.3	5663.0	6699.8	4677.9
EU734961.1	311415	199.0	332.2	1058.7	112.6	968.5	396.1
AY123813.1	73969	5239.7	9387.6	6435.8	5167.7	8734.5	6406.5
L35505.1	6517	1197.8	1171.7	3670.1	1637.1	965.5	1852.2

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AF363291.1 gg_id:40900 Nitrosovibrio sp. str. RY6A
EU287131.1 gg_id:245816 Pacific arctic surface sediment clone P13-38
X90820.1 gg_id:6538 Nitrosospira sp str. AHB1
AJ005545.1 gg_id:6518 Nitrosospira sp. F3
AY631270.1 gg_id:106086 Nitrosovibrio sp. FJI423
AF363290.1 gg_id:43839 Nitrosovibrio sp. str. RY3C
M96396.1 gg_id:6503 Nitrosospira briensis
GQ396891.1 gg_id:592669 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EU676432.1 gg_id:288399 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
AF177427.1 gg_id:37585 Acanthamoeba sp. UWC12 symbiont
AF177425.1 gg_id:43515 Acanthamoeba sp. Page 23 symbiont
AF352385.1 gg_id:29264 Acanthamoeba sp. TUMSJ-226 symbiont
DQ280369.1 gg_id:144094 Microvirgula sp. str. HW7
EU708500.1 gg_id:296975 and Situ Quantification Arsenite Oxidizing Denitrifying Enrichment anoxic arsenite ox
AF331975.1 gg_id:66610 Azoarcus sp. str. HxN1
Y13222.1 gg_id:6771 Azoarcus sp. str. 22Lin
NR_024970.1 gg_id:543017 Azoarcus toluclasticus str. MF63; ATCC 700605
AF123075.1 gg_id:6778 Azoarcus tolulyticus str. BL11
AF123076.1 gg_id:6779 Azoarcus toluclasticus str. MF7
L33687.1 gg_id:6804 Azoarcus tolulyticus str. Td-1
L33693.1 gg_id:6782 Azoarcus tolulyticus str. Td-3
L33692.1 gg_id:6784 Azoarcus tolulyticus str. Td-21
DQ264504.1 gg_id:141528 universal microarray broader than typical library when sampling subsurface groundv
DQ264480.1 gg_id:142574 universal microarray broader than typical library when sampling subsurface groundv
L33688.1 gg_id:6766 Azoarcus tolulyticus str. Td-15
AB234249.1 gg_id:148299 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
DQ264419.1 gg_id:143835 universal microarray broader than typical library when sampling subsurface groundv
L33689.1 gg_id:6781 Azoarcus tolulyticus str. Td-17
DQ264565.1 gg_id:142083 universal microarray broader than typical library when sampling subsurface groundv
AF229861.1 gg_id:35148 Azoarcus tolulyticus str. 2FB6
EU528179.1 gg_id:286700 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AJ630292.1 gg_id:100647 Azonexus fungiphilus
GU056304.1 gg_id:557513 Anoxic Oxidation Arsenite Arsenate linked Chlorate Reduction returned actived slud
AF011347.1 gg_id:6714 Azospira oryzae str. 6a3
AY235689.1 gg_id:106890 Nitrogen-fixation strains wild rice
AY171616.1 gg_id:77627 Dechlorosoma sp. str. AH
DQ863512.1 gg_id:165690 Azospira oryzae str. N1
AF170348.1 gg_id:6722 Azospira oryzae str. PS
AY277622.1 gg_id:101136 Azospira oryzae str. GR-1
FJ391490.1 gg_id:367951 primers targeting Gallionella- neutrophilic oxidizers enrichments and soils iron rich irr
AF011349.1 gg_id:6675 Azovibrio sp. str. BS20-3

AF363291.1	40900	5330.0	5539.7	5887.7	7492.9	4748.4	8693.2
EU287131.1	245816	7501.8	5561.0	7511.8	8751.0	5360.2	7208.2
X90820.1	6538	4684.9	4937.0	9775.7	6960.9	6591.0	5967.5
AJ005545.1	6518	18246.3	20094.7	22034.0	17069.9	16562.9	19889.9
AY631270.1	106086	10140.0	11141.1	10293.1	6686.8	10724.9	8936.8
AF363290.1	43839	10412.7	7846.3	7224.2	10122.6	11027.3	16138.8
M96396.1	6503	1530.3	1600.3	5205.0	5048.7	2203.8	3710.4
GQ396891.1	592669	8156.1	5388.5	7381.5	9986.0	7545.4	8297.9
EU676432.1	288399	7543.9	6688.1	6652.4	9566.2	7492.6	8108.1
AF177427.1	37585	11890.5	9702.6	11525.9	12701.4	7762.4	11410.1
AF177425.1	43515	2397.5	3864.4	5185.2	6350.5	3226.8	6261.1
AF352385.1	29264	9631.5	9076.7	6798.8	10974.4	9729.8	11665.7
DQ280369.1	144094	4813.2	4566.7	10631.9	6999.2	3491.8	4742.6
EU708500.1	296975	6383.1	5657.4	12552.8	8963.2	4824.1	5221.4
AF331975.1	66610	3194.9	3652.2	6030.1	4838.1	4428.7	5309.7
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NR_024970.1	543017	10913.7	5973.6	17465.0	11484.6	6398.8	6950.8
AF123075.1	6778	5589.8	4071.8	8907.5	5977.0	3950.1	4681.8
AF123076.1	6779	1840.8	2830.2	3250.7	1165.0	1338.1	1747.5
L33687.1	6804	7566.9	5875.9	12779.6	7915.3	3773.7	5752.8
L33693.1	6782	7626.8	6639.7	7779.6	5577.6	6868.5	6055.9
L33692.1	6784	6857.3	4855.3	13902.8	9293.0	5439.4	5953.0
DQ264504.1	141528	11041.5	5290.2	12623.0	11283.0	4991.5	6732.0
DQ264480.1	142574	7577.7	5189.6	10579.2	5194.4	2803.7	4017.6
L33688.1	6766	2868.7	2574.2	10794.0	4538.7	3157.2	2854.0
AB234249.1	148299	9543.4	6400.0	13264.9	11553.4	7694.7	8091.5
DQ264419.1	143835	6748.5	3780.7	12411.7	7591.9	6556.5	8208.6
L33689.1	6781	5879.3	1909.8	8111.6	5695.9	1969.2	3413.2
DQ264565.1	142083	5446.7	5426.5	13177.7	6644.6	6647.8	6400.0
AF229861.1	35148	4719.7	3776.4	10035.4	5278.0	5855.1	5939.5
EU528179.1	286700	11120.7	11580.3	11017.3	9185.2	12847.0	10411.3
AJ630292.1	100647	5235.0	5135.7	11543.9	7206.6	5021.6	4065.7
GU056304.1	557513	4178.0	4101.8	5216.7	4480.1	2814.9	3521.3
AF011347.1	6714	2285.0	3754.7	10300.7	4203.1	6373.7	5469.1
AY235689.1	106890	1378.4	1839.3	7625.1	2432.4	4505.9	4068.5
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DQ863512.1	165690	4768.0	6245.1	12063.4	5359.0	7376.9	7111.2
AF170348.1	6722	6788.7	4932.6	9695.6	7500.8	10030.1	7308.2
AY277622.1	101136	5046.0	6206.4	12173.4	6151.9	9016.9	7759.1
FJ391490.1	367951	9655.2	5046.9	8784.8	9534.1	7536.4	6942.4
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NC_007298.1 gg_id:203562 Dechloromonas aromatica str. RCB
FJ535057.1 gg_id:591896 Enhancement protein conversion volatile fatty acids accumulation during addition: ef
DQ640664.1 gg_id:233934 full-scale EBPR sludge clone Skagenf42
GQ340232.1 gg_id:551430 Prokaryotic Marathonas Reservoir Greece water column clone VE07-68-BAC
AM084133.1 gg_id:140097 Dechloromonas sp. str. R-28400
AB240507.1 gg_id:142587 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
FJ719082.1 gg_id:531877 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p04_E04
EF515635.1 gg_id:224951 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
DQ376553.1 gg_id:153255 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin
CU466914.1 gg_id:319502 Evry wastewater treatment plant anoxic basin clone
CU920167.1 gg_id:572334 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU466920.1 gg_id:304463 Evry wastewater treatment plant anoxic basin clone
AB240296.1 gg_id:144181 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
CU466858.1 gg_id:344521 Evry wastewater treatment plant anoxic basin clone
FJ444762.1 gg_id:542590 Cotton Rhizosphere cotton rhizosphere clone 4y-107
CU926684.1 gg_id:554053 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
Y17060.1 gg_id:6706 Ferribacterium limneticum str. cda-1
DQ296471.1 gg_id:161279 Microbial dissection quinoline-degradation lab-scale anaerobic biofilm reactor quino
CU466895.1 gg_id:319055 Evry wastewater treatment plant anoxic basin clone
DQ923115.1 gg_id:163080 Methyloversatilis universalis str. 500
FJ167509.1 gg_id:333442 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
FJ902588.1 gg_id:568555 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
FM207922.1 gg_id:305052 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
DQ088734.1 gg_id:137170 subsurface clone BE16FW031601GDW_hole1-11
AB234251.1 gg_id:150027 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
DQ676301.1 gg_id:224877 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
FM207901.1 gg_id:328865 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
DQ327692.1 gg_id:166580 Biological filtration limits carbon availability affects downstream biofilm formation a
AY945886.1 gg_id:146463 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal
FJ484883.1 gg_id:511775 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
DQ088748.1 gg_id:129402 subsurface clone BE325FW032701CTS_hole1-85
FM207903.1 gg_id:327175 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
FM207916.1 gg_id:351540 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
EF363051.1 gg_id:268998 Microbial life within saline fluid Continental Deep Drilling German continental deep g
AB252920.1 gg_id:171974 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 010
AY879297.1 gg_id:111577 Denitratisoma oestradiolicum str. AcBE2-1
FM207918.1 gg_id:344874 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
FJ485121.1 gg_id:533665 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat
DQ676390.1 gg_id:222171 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
GQ340363.1 gg_id:538380 Prokaryotic Marathonas Reservoir Greece water column clone VE08-161-BAC
EF205275.1 gg_id:200507 Arctic gold mine fracture water clone Lupin-1130m-1-MDA-ubp1

NC_007298.1	203562	12893.4	10275.8	19449.8	14981.5	9358.0	10341.4
FJ535057.1	591896	6078.5	3998.7	8798.1	7431.2	5845.1	5179.1
DQ640664.1	233934	8108.6	7385.2	6463.6	7723.5	8632.3	7009.6
GQ340232.1	551430	2846.9	2626.1	6936.6	4578.0	1555.2	1991.3
AM084133.1	140097	3464.1	1626.4	3367.4	4500.6	1369.2	1440.9
AB240507.1	142587	1782.6	1982.8	11143.1	2419.6	4844.0	1959.1
FJ719082.1	531877	5262.8	4367.6	15673.9	6441.6	9685.9	6487.2
EF515635.1	224951	4573.8	6335.4	5016.2	5096.3	5032.4	3899.9
DQ376553.1	153255	8099.0	7748.3	12500.2	8057.4	9055.4	8371.0
CU466914.1	319502	8489.7	9692.6	11332.4	9776.9	13633.1	9695.0
CU920167.1	572334	16312.1	6878.3	18659.4	13971.4	9831.3	8206.3
CU466920.1	304463	8493.3	5281.4	11043.0	10422.9	7145.0	6608.8
AB240296.1	144181	201.4	193.1	508.3	357.3	244.6	269.8
CU466858.1	344521	18013.0	13290.0	15593.5	14815.2	13588.5	13531.7
FJ444762.1	542590	7056.1	4708.3	13765.6	8614.7	7793.3	5091.7
CU926684.1	554053	7086.2	5484.6	3929.8	5110.4	3752.4	3979.3
Y17060.1	6706	7344.3	8390.8	16213.1	9580.7	5325.9	5529.9
DQ296471.1	161279	1238.7	1016.2	4159.6	2336.9	2585.9	1416.7
CU466895.1	319055	3039.4	3294.5	26877.4	5375.3	8030.1	3416.5
DQ923115.1	163080	2123.1	2951.8	4564.8	2938.1	3214.2	3080.0
FJ167509.1	333442	6113.7	8084.0	7717.6	5078.0	5648.1	4794.0
FJ902588.1	568555	5372.9	6235.1	10458.1	5907.4	4451.0	6427.7
FM207922.1	305052	14819.4	12550.1	13317.7	11796.8	13934.2	12050.1
DQ088734.1	137170	3067.5	1699.3	4130.3	5115.0	1681.6	2122.8
AB234251.1	150027	844.2	446.0	3633.0	1788.1	792.1	297.7
DQ676301.1	224877	6180.3	3682.7	16029.1	10066.0	6718.1	6660.4
FM207901.1	328865	3997.5	2881.8	6977.3	5930.4	3677.3	4349.2
DQ327692.1	166580	1499.4	2230.7	5772.7	2574.9	2995.0	3194.2
AY945886.1	146463	167.6	183.4	122.6	199.2	69.8	117.0
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DQ088748.1	129402	10324.7	8147.5	11059.3	14093.5	9982.8	9948.6
FM207903.1	327175	16772.4	15418.2	22738.5	14174.3	16552.0	14606.7
FM207916.1	351540	8842.4	8015.3	19968.3	9339.8	9244.3	8519.2
EF363051.1	268998	6458.1	8272.3	9814.7	4853.8	6455.6	7189.9
AB252920.1	171974	13166.1	13873.8	9458.9	10887.9	14107.0	14645.2
AY879297.1	111577	1222.8	1735.7	2803.9	2491.9	1222.6	1846.7
FM207918.1	344874	5391.0	4237.9	9540.6	8101.1	4396.7	3253.9
FJ485121.1	533665	5763.2	4470.9	8854.1	5273.1	3773.9	4021.6
DQ676390.1	222171	9083.4	9882.7	7588.3	8878.1	5979.9	6747.8
GQ340363.1	538380	7886.0	6341.1	14423.1	10341.4	8409.5	7829.5
EF205275.1	200507	8323.2	7192.0	13895.4	10669.5	10902.1	8105.7

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AY235684.1 gg_id:106107 Nitrogen-fixation strains wild rice
AJ306683.1 gg_id:27286 Sterolibacterium denitrificans str. Chol-1S
FJ391504.1 gg_id:369022 primers targeting Gallionella- neutrophilic oxidizers enrichments and soils iron rich irr
DQ836749.1 gg_id:163176 attached biomass denitrifying bioreactor clone DB-5
AM934804.1 gg_id:556892 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FM207927.1 gg_id:325823 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
FM207953.1 gg_id:304406 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
DQ532120.1 gg_id:161420 Ultramicrobacter hongkongensis str. 5a1
DQ676425.1 gg_id:226206 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AM268369.1 gg_id:191997 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
AB186837.1 gg_id:107618 polychlorinated dioxin dechlorinating microcosm clone TSBW06
AY532566.1 gg_id:101212 uranium-contaminated aquifer clone 1013-28-CG13
AF234757.1 gg_id:51803 sludge clone S40
AF204243.1 gg_id:31185 P+ sludge clone GC24
AY762627.1 gg_id:108150 gold mine clone DSBACT86
AB378589.1 gg_id:271761 dominate denitrification nitrate- succinate-ammended stable istope probing 13C fra
EF590007.2 gg_id:228477 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
AF072922.1 gg_id:6533 nitrifying/denitrifying industrial activated sludge clone S28 S28
AY328574.1 gg_id:89345 drinking water system simulator clone HOClCi25
GU454941.1 gg_id:530591 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
EF492892.1 gg_id:236435 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EU037206.1 gg_id:239439 Hot Spring Microbial Mat Khir Ganga India hot spring microbial mat clone MO91
DQ984607.1 gg_id:235493 LY oil-contaminated soil clone LYC108
FM204950.1 gg_id:547160 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
EU835438.1 gg_id:352426 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B09
DQ464135.1 gg_id:157026 acid mine drainage clone D3-25
FM207915.1 gg_id:349221 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr
AB179684.1 gg_id:106337 groundwater 0.2 m-captured fraction clone KNA6-EB04
DQ988263.1 gg_id:190625 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with
AB252918.1 gg_id:167769 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 195
EF565160.1 gg_id:246262 'Candidatus accumulibacter' structure enhanced biological phosphorus removal sludg
FJ356026.1 gg_id:366769 Targeted FACS enrichment groups lab scale systems anaerobic:aerobic lab-scale EBPR
GU250852.1 gg_id:578062 Anaerobic biodegradation branched hydrocarbon biomarker analog pristane waste
D16210.1 gg_id:6712 Rhodocyclus tenuis str. SW18
D16209.1 gg_id:6713 Rhodocyclus tenuis str. DSM110
AY297807.1 gg_id:88575 waterlogged archaeological wood clone pACH91
AF227840.1 gg_id:26639 str. 51885
DQ640677.1 gg_id:230074 full-scale EBPR sludge clone Skagenf18
AY706424.1 gg_id:100543 TCE-contaminated groundwater clone G1a
Y17601.1 gg_id:6721 Propionivibrio dicarboxylicus str. DSM 5885
AB062831.1 gg_id:54073 termite gut homogenate clone BCf6-08

AY235684.1	106107	3902.6	4770.5	9252.6	6975.2	4707.0	7137.8
AJ306683.1	27286	81.5	103.1	2501.0	401.8	330.5	100.5
FJ391504.1	369022	2157.8	2285.2	10974.9	3789.9	4918.6	3203.3
DQ836749.1	163176	17325.8	15626.2	10956.4	15027.7	13601.9	14212.7
AM934804.1	556892	2144.8	2390.5	4801.4	2253.9	1782.0	2274.4
FM207927.1	325823	8666.7	8715.1	14834.6	9610.5	9344.7	8439.4
FM207953.1	304406	7613.7	7093.7	9638.8	5977.2	5938.9	4458.9
DQ532120.1	161420	2856.3	3833.4	10038.3	5179.4	10819.8	6976.2
DQ676425.1	226206	489.4	725.0	2996.5	2622.7	2071.1	905.3
AM268369.1	191997	2751.7	2117.6	4468.9	3446.4	3404.6	2621.1
AB186837.1	107618	8975.7	8252.8	11732.3	10257.5	8234.4	7552.1
AY532566.1	101212	10490.9	8655.4	20295.1	10617.8	12583.1	9722.4
AF234757.1	51803	8877.5	6499.8	3760.9	8364.5	10710.7	11421.3
AF204243.1	31185	24.8	143.1	230.0	100.1	159.8	42.4
AY762627.1	108150	4921.7	4384.2	5492.5	5711.6	4552.9	2500.6
AB378589.1	271761	2089.1	2358.7	5983.6	3260.9	2805.8	4169.4
EF590007.2	228477	11225.7	11403.1	13043.0	12099.2	13567.1	11914.3
AF072922.1	6533	4919.0	3489.9	7996.7	8306.2	3063.3	4944.2
AY328574.1	89345	244.2	421.4	1411.0	269.1	1619.1	955.7
GU454941.1	530591	2042.9	2509.2	3984.7	4156.1	2061.8	4722.9
EF492892.1	236435	1962.9	2124.9	12473.0	6242.1	3593.5	3140.7
EU037206.1	239439	5077.8	4750.8	4164.6	9557.8	6079.4	5876.1
DQ984607.1	235493	11615.8	8875.8	18091.7	13650.9	10979.3	9155.9
FM204950.1	547160	12248.6	10300.5	12144.0	10748.7	9168.7	9042.6
EU835438.1	352426	4129.8	4966.8	3545.6	5210.2	4087.7	4590.7
DQ464135.1	157026	145.1	240.7	286.5	583.5	126.0	125.2
FM207915.1	349221	12945.7	11831.7	12516.4	11114.8	11156.3	8935.3
AB179684.1	106337	1992.4	2295.0	4973.6	3789.5	3043.4	2619.3
DQ988263.1	190625	3884.1	3624.4	3638.7	5142.0	3588.0	2698.0
AB252918.1	167769	18177.9	16430.1	28113.4	19702.9	15617.5	13807.5
EF565160.1	246262	4015.7	4323.1	11820.9	7339.4	5387.9	9616.0
FJ356026.1	366769	7647.4	8390.1	12350.5	11332.6	9507.0	10189.6
GU250852.1	578062	3169.9	4654.2	6608.4	4175.8	4800.5	4532.6
D16210.1	6712	2921.0	2886.9	5891.4	4424.3	3425.9	4854.5
D16209.1	6713	7921.3	5046.7	9541.4	7735.7	5871.0	6584.4
AY297807.1	88575	6102.0	5770.6	17868.1	8007.2	6555.0	7049.7
AF227840.1	26639	739.7	1135.8	4802.3	1507.8	2379.1	1730.7
DQ640677.1	230074	18723.6	17969.7	18348.6	16806.3	19628.7	16515.0
AY706424.1	100543	10939.8	10056.6	5440.2	14314.3	12791.7	13809.5
Y17601.1	6721	1053.6	2182.5	7262.8	2981.5	1443.1	2019.9
AB062831.1	54073	1978.6	3286.2	2325.1	5344.3	1581.2	2419.4

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AF502231.1 gg_id:59337 EBPR sludge clone HP1A26
AB240294.1 gg_id:143468 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AB089103.1 gg_id:78240 termite gut homogenate clone Rs-K54
NR_024855.1 gg_id:545495 Propionivibrio pelophilus str. asp 66; DSM 12018
AY064179.1 gg_id:65492 EBPR sludge clone UCTN173
AF255631.1 gg_id:36331 EBPR sludge clone Ebpr16
DQ087192.1 gg_id:134476 clone HE018
AY691423.1 gg_id:105089 Rhodocyclus sp. str. HOD 5
AF229868.1 gg_id:18623 Thauera aromatica str. 4FB2
AF229867.1 gg_id:42293 Thauera aromatica str. 4FB1
AF229882.1 gg_id:69798 Thauera aromatica str. 3CB3
AF123264.1 gg_id:6759 Thauera chlorobenzoica str. 3CB-1
AF229887.1 gg_id:36677 Thauera aromatica str. 3BB1
AJ315678.1 gg_id:25264 Thauera phenylacetica str. B4P
AJ315677.1 gg_id:40990 Thauera aminoaromatica str. S2
U95176.1 gg_id:6763 Thauera aromatica str. T1
AY548757.1 gg_id:111927 Thauera sp. str. Cin34
EU434525.1 gg_id:273528 Thauera phenylacetica str. b208
AY098637.2 gg_id:71611 industrial-phenol-degrading community clone MM1 sp.
DQ018816.1 gg_id:131190 anaerobic swine lagoon clone C-147
AJ505850.1 gg_id:58572 Thauera sp. str. PIV-1
EU434574.1 gg_id:265716 Thauera aromatica str. b66
FJ900965.1 gg_id:513787 Polymorphism microbial reservoirs water cut stage oil field clone G-3
AM982629.2 gg_id:279478 microbial and slurry pig saw dust spent bedding clone PISD-AJG10
AB210048.1 gg_id:122645 mini plant Run 5 Nippon Steel Research Engineering Center clone nsmpV06
CU466853.1 gg_id:346949 Evry wastewater treatment plant anoxic basin clone
AJ853609.1 gg_id:111043 landfill leachate clone GZKB116
AY823976.1 gg_id:145956 Investigation Acetate-Fed Denitrifying Microbial Stable Isotope Probing Full-Cycle an
X68491.1 gg_id:6756 Thauera selenatis str. Ax
EF205256.1 gg_id:197834 Thauera sp. 'CJAOPY3 (T-II)' str. CJAOPY3 (T-II)
FJ825447.1 gg_id:569266 Microbial during start-up mesophilic biogas plant clone 112_BE3_37
AY823967.1 gg_id:145778 Investigation Acetate-Fed Denitrifying Microbial Stable Isotope Probing Full-Cycle an
AY570693.1 gg_id:108565 Thauera sp. Al7
Y17590.1 gg_id:6761 Thauera mechernichensis str. TL1
EU434467.1 gg_id:271936 Thauera aminoaromatica str. a241
AY945863.1 gg_id:149463 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal
AY945915.1 gg_id:145574 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal
Y17591.1 gg_id:6762 Thauera selenatis str. ATCC 55363T
AJ005816.1 gg_id:6747 Thauera linaloolentis str. 47Lol
AM268367.1 gg_id:179901 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
DQ018794.1 gg_id:133087 anaerobic swine lagoon clone C-38

AF502231.1	59337	140.9	368.9	1011.6	261.5	685.2	898.3
AB240294.1	143468	4039.2	4468.2	9651.7	8118.2	6697.4	7591.4
AB089103.1	78240	4680.2	2124.1	2083.3	5066.4	1122.6	1823.9
NR_024855.1	545495	1682.0	1049.8	5165.7	4079.4	1840.2	2039.5
AY064179.1	65492	14479.3	12675.3	19254.0	15797.9	12550.4	14526.9
AF255631.1	36331	2077.6	2980.9	6178.9	5137.9	1631.7	3819.9
DQ087192.1	134476	2637.7	1447.5	1952.6	3617.5	849.0	1103.9
AY691423.1	105089	1486.0	1222.1	5060.8	1860.7	2271.7	2193.7
AF229868.1	18623	14754.2	12484.6	11381.1	13927.1	12317.8	10575.3
AF229867.1	42293	10281.6	10216.8	9072.0	11120.3	8066.0	7998.2
AF229882.1	69798	3882.4	2447.6	1947.6	2800.2	1577.1	3090.5
AF123264.1	6759	4314.5	4326.6	5350.6	5286.4	3419.3	4479.1
AF229887.1	36677	7929.0	5836.2	7890.1	7629.9	4158.5	5679.7
AJ315678.1	25264	461.2	633.2	1193.6	1679.4	307.8	409.8
AJ315677.1	40990	3922.1	3429.4	7290.5	7320.7	3958.2	2381.3
U95176.1	6763	4584.4	5335.3	6460.1	608.1	2497.8	2071.5
AY548757.1	111927	4376.3	4021.9	6070.1	8849.0	3129.5	4340.3
EU434525.1	273528	8684.8	6977.9	10170.2	7555.0	8269.6	6487.9
AY098637.2	71611	1058.4	606.4	675.1	499.3	254.9	329.7
DQ018816.1	131190	3019.1	1927.7	5006.6	3612.3	2373.3	3368.7
AJ505850.1	58572	4935.6	3434.4	9096.5	6024.3	3606.5	4746.5
EU434574.1	265716	10815.5	10641.6	17029.6	12024.8	10005.6	8889.3
FJ900965.1	513787	1971.8	1840.2	3875.7	4968.3	1140.8	2391.6
AM982629.2	279478	10512.0	10905.8	8770.5	11684.7	7964.7	10873.4
AB210048.1	122645	45.0	88.9	253.1	200.6	94.6	31.9
CU466853.1	346949	1778.6	1528.9	3427.3	4218.5	1228.5	868.6
AJ853609.1	111043	1065.6	938.9	340.1	1831.2	1230.0	1032.4
AY823976.1	145956	1743.8	1881.2	3195.7	2206.4	3270.6	1646.1
X68491.1	6756	864.3	1930.0	4316.5	587.7	1680.0	1151.8
EF205256.1	197834	14957.4	13377.4	21641.0	15164.2	12197.7	11839.1
FJ825447.1	569266	2801.2	2986.6	3371.2	2296.4	1716.3	2160.1
AY823967.1	145778	5995.0	7177.8	12708.1	7111.8	7631.8	6078.9
AY570693.1	108565	3747.1	2555.9	2476.4	4716.0	1410.0	1712.4
Y17590.1	6761	6381.6	2937.2	11440.5	8053.7	2382.2	3737.7
EU434467.1	271936	3006.6	1467.1	2118.3	4006.1	1048.2	2110.0
AY945863.1	149463	7307.3	3967.6	5953.6	7231.3	4710.3	6836.5
AY945915.1	145574	2381.7	1823.7	2350.5	1720.7	1463.2	915.2
Y17591.1	6762	3219.7	4814.6	10034.7	6229.9	6709.4	4237.3
AJ005816.1	6747	1797.8	1962.1	4484.0	5461.3	2194.2	3682.4
AM268367.1	179901	3930.0	3198.1	1717.3	3473.3	1060.6	2890.9
DQ018794.1	133087	6009.3	5721.2	8317.2	5790.4	5388.0	5672.1

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FJ901012.1 gg_id:552697 Polymorphism microbial reservoirs water cut stage oil field clone G-60
AY945909.1 gg_id:147554 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal r
GQ107403.1 gg_id:424310 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
EU104249.1 gg_id:335484 Evidence Comamonadaceae determinants settling performance activated sludge clo
AM268359.1 gg_id:196002 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
GQ093262.1 gg_id:442735 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
AB192185.1 gg_id:144844 termite gut homogenate clone RsTz-39
AY265878.1 gg_id:82517 perchlorate-reducing PMC
GQ100922.1 gg_id:463566 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ086556.1 gg_id:424472 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29
AY124797.1 gg_id:69212 Dechloromonas sp. str. LT-1
DQ376566.1 gg_id:152042 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin
AB369190.1 gg_id:254556 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
AF072921.1 gg_id:6799 nitrifying/denitrifying industrial activated sludge clone S23 S23
AF072918.1 gg_id:6786 nitrifying/denitrifying industrial activated sludge clone S3 S3
DQ640700.1 gg_id:231550 full-scale EBPR sludge clone Skagenf76
FJ823914.1 gg_id:526353 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
GQ024542.1 gg_id:485128 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123e11c1
AY947989.1 gg_id:142103 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl
AF072919.1 gg_id:6787 nitrifying/denitrifying industrial activated sludge clone H25 H25
GQ093869.1 gg_id:399333 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
EU015084.1 gg_id:236679 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
EF648064.1 gg_id:241562 dynamics during produced water treatment aerobic activated sludge clone HB61
EU133837.1 gg_id:240971 tallgrass prarie soil clone FFCH15186
AY160865.1 gg_id:96448 termite intestinal tract clone COB P5-5
AB024934.1 gg_id:21532 Sphingomonas sp. A1
DQ836761.1 gg_id:167461 attached biomass denitrifying bioreactor clone DB-86
FJ478739.1 gg_id:511268 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ974114.1 gg_id:245301 Azospira restricta str. SUA2
FJ374246.1 gg_id:362367 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
AF204246.1 gg_id:50481 EBPR sludge clone SBRH147
GQ085455.1 gg_id:431512 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw275h11
EU133861.1 gg_id:249511 tallgrass prarie soil clone FFCH8183
AY007722.1 gg_id:29482 Quadricoccus australiensis str. Ben 117; NCIMB 13738; CIP 107055
AY212577.1 gg_id:99384 water 10 m downstream manure clone 126ds10
EU015096.1 gg_id:236222 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
AB288886.1 gg_id:201491 termite gut homogenate clone BOf2-09
AB487233.1 gg_id:562019 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
FJ167461.1 gg_id:353414 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
AB237674.1 gg_id:140535 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW
AJ582195.1 gg_id:93931 soil near uranium mill tailings clone Gitt-GS-125

FJ901012.1	552697	11139.3	13676.5	9606.3	8751.8	10054.8	10141.0
AY945909.1	147554	3107.2	2982.1	8215.0	5156.1	1646.9	3202.0
GQ107403.1	424310	3240.6	2734.2	4643.5	6249.0	3357.9	4190.7
EU104249.1	335484	5228.1	4103.7	8810.8	9730.3	1914.8	4191.1
AM268359.1	196002	2771.4	3164.2	1375.3	4095.5	1859.4	3153.9
GQ093262.1	442735	5671.9	4763.1	6355.0	6209.0	6298.9	6917.7
AB192185.1	144844	458.0	301.7	1815.2	773.8	297.7	615.7
AY265878.1	82517	2819.8	2816.0	2662.5	2192.8	4944.7	2567.2
GQ100922.1	463566	2325.5	2542.2	5633.9	3280.7	4557.0	3019.5
GQ086556.1	424472	5829.8	4673.0	8012.7	7184.3	8488.1	7740.3
AY124797.1	69212	2554.7	3068.6	7776.3	2922.6	3021.8	5134.9
DQ376566.1	152042	9005.5	5361.0	12627.5	8539.4	6370.8	6175.0
AB369190.1	254556	5919.0	3697.0	10110.8	6894.6	3081.2	4156.6
AF072921.1	6799	14591.4	16818.7	18079.5	12653.0	20211.9	14404.8
AF072918.1	6786	6436.5	7262.8	8573.4	5937.2	3399.0	5348.7
DQ640700.1	231550	8660.7	9846.2	10321.2	10340.1	11824.4	11923.3
FJ823914.1	526353	2562.2	3125.2	9380.7	5862.9	5062.7	5295.0
GQ024542.1	485128	7590.4	6069.0	11503.4	8704.2	8867.3	7395.0
AY947989.1	142103	1116.7	1140.9	4535.4	3430.0	1157.8	1338.0
AF072919.1	6787	6918.7	6841.6	4112.0	6976.8	10566.7	8306.9
GQ093869.1	399333	7595.3	5648.4	6092.6	8179.0	4115.5	5168.1
EU015084.1	236679	9099.9	6036.1	12468.7	8821.2	4567.3	6034.1
EF648064.1	241562	2046.5	3282.6	10207.1	2899.4	4127.1	1951.8
EU133837.1	240971	1241.8	1562.5	4820.2	1457.8	4021.2	1361.2
AY160865.1	96448	142.5	141.5	876.3	397.9	977.3	314.1
AB024934.1	21532	79.5	198.9	612.4	191.9	490.4	292.9
DQ836761.1	167461	6132.8	4566.5	11101.5	8397.2	3897.5	4588.7
FJ478739.1	511268	9323.3	8757.9	10388.4	8784.5	5446.3	7905.7
DQ974114.1	245301	2757.5	4979.2	6319.2	5147.1	4282.7	4295.5
FJ374246.1	362367	3462.1	2417.9	9911.3	8506.9	5824.6	4505.8
AF204246.1	50481	480.5	351.6	1414.5	572.3	1302.5	856.6
GQ085455.1	431512	11780.0	14453.2	11420.9	12175.7	15917.4	15880.9
EU133861.1	249511	2704.7	2396.4	2352.5	2415.4	664.0	1997.0
AY007722.1	29482	674.5	372.7	522.8	797.8	401.5	381.1
AY212577.1	99384	4456.0	4913.3	6107.7	4513.9	2421.5	3031.4
EU015096.1	236222	9490.6	7304.7	15697.7	14602.5	8682.2	8540.4
AB288886.1	201491	210.5	219.1	271.1	324.7	1020.8	139.2
AB487233.1	562019	6975.5	7174.6	11798.0	8666.2	6597.0	7079.1
FJ167461.1	353414	112.6	91.4	468.0	173.8	200.1	147.2
AB237674.1	140535	2538.2	2100.6	7668.7	4317.2	1657.7	2770.6
AJ582195.1	93931	92.8	171.0	243.5	208.3	480.7	223.6

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AM268344.1 gg_id:186145 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
EU283471.1 gg_id:277656 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1227
GQ979961.1 gg_id:589706 microbial biofilm soluble nitrate reducing bioreactor clone SRC_NRB032
AB166784.1 gg_id:107623 EBPR sludge clone UTFS-OF08-18
AB456210.1 gg_id:553408 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o\
AM982545.1 gg_id:278568 microbial and slurry pig straw spent bedding clone PIST-AGC10
AB198538.1 gg_id:135858 termite gut wall fraction clone RsW02-065
DQ088747.1 gg_id:131456 subsurface clone BE23FW031301A4RD-1
FJ374248.1 gg_id:364266 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
GQ105914.1 gg_id:447649 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw.
DQ395985.1 gg_id:151035 deep-sea octacoral clone ctg_CGOGA28
AJ005817.1 gg_id:6750 Thauera terpenica str. 58Eu
AB192235.1 gg_id:141727 termite gut homogenate clone RsTu1-85
AJ863432.1 gg_id:120677 poplar tree microcosm rhizoplane flooded clone 23RPF22
GQ098414.1 gg_id:416580 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw559c
AY188298.1 gg_id:80896 marine? clone KD2-110
GQ104731.1 gg_id:415263 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF192878.1 gg_id:202891 sediments temperate artificial lake Rapel reservoir sediment clone Rap1_1B
AM268363.1 gg_id:185155 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
FJ439857.1 gg_id:513084 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M3
GQ103332.1 gg_id:463253 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw699b0:
FJ478630.1 gg_id:569356 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ979958.1 gg_id:532793 microbial biofilm soluble nitrate reducing bioreactor clone SRC_NRB029
AB166882.1 gg_id:104301 Azonexus sp. str. Slu-05
GU454933.1 gg_id:520944 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
AB192066.1 gg_id:143225 termite gut homogenate clone M1PL1-62
GQ065924.1 gg_id:397799 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw94e08c
GU454955.1 gg_id:525767 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
DQ517100.1 gg_id:160794 Cultivation-intensive study ephemeral hypereutrophic aquatic microbial Mojave Des
GU222238.1 gg_id:586616 Anaerobic biodegradation branched hydrocarbon biomarker analog pristane wastew
AY770497.1 gg_id:143561 and isolation that grow on 12-dichloroethane under nitrate reducing conditions sedir
AB486739.1 gg_id:585587 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
GQ231337.1 gg_id:560504 -stable isotope probing integrated metagenomics biphenyl dioxygenase genes polyc
AF011343.1 gg_id:6783 Azoarcus communis str. SWub3
FJ823940.1 gg_id:529251 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
AY662036.1 gg_id:136814 uranium-contaminated groundwater clone 300I-F02
FJ479338.1 gg_id:539491 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ108087.1 gg_id:430940 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU244087.1 gg_id:360080 16SrRNA probes river Leine sediment clone sl1373
EF019494.1 gg_id:214657 aspen rhizosphere clone Elev_16S_763
AB049763.1 gg_id:27927 Denitromonas aromaticus str. AS-7

AM268344.1	186145	1171.0	1167.8	5608.4	3492.7	1423.7	988.4
EU283471.1	277656	5921.2	6489.0	11615.1	8962.0	8346.8	8987.8
GQ979961.1	589706	3348.3	5642.3	8466.2	4027.3	8363.0	6987.1
AB166784.1	107623	11420.4	9817.0	9118.8	11751.3	11383.5	12498.9
AB456210.1	553408	545.6	578.4	1599.5	456.9	1774.8	872.0
AM982545.1	278568	2937.0	3329.6	7030.3	4203.6	3358.9	6195.9
AB198538.1	135858	148.3	311.2	234.7	328.2	86.5	72.9
DQ088747.1	131456	132.6	128.1	315.1	307.1	559.8	110.9
FJ374248.1	364266	4648.9	4849.9	9395.9	7318.7	5739.2	6683.9
GQ105914.1	447649	7202.1	8113.7	11661.0	8510.3	11082.9	8037.9
DQ395985.1	151035	54.2	60.4	273.5	87.5	102.3	69.7
AJ005817.1	6750	1431.6	1810.5	4248.1	2615.2	2330.7	1736.7
AB192235.1	141727	378.9	438.5	1329.4	1762.4	551.3	895.0
AJ863432.1	120677	10113.1	7024.6	13709.6	11287.6	6319.9	6743.0
GQ098414.1	416580	2729.5	2419.0	4584.2	2655.7	2294.8	1970.9
AY188298.1	80896	14171.1	14236.3	12340.3	12253.8	12212.4	12533.1
GQ104731.1	415263	7673.9	8454.2	10944.3	9379.3	11341.4	9880.1
EF192878.1	202891	87.1	89.9	105.5	292.6	133.4	220.5
AM268363.1	185155	4107.6	3026.1	7032.1	6833.1	2230.2	3169.5
FJ439857.1	513084	1097.7	1589.7	2422.1	1408.5	1027.0	936.6
GQ103332.1	463253	9704.7	6356.5	12551.8	10070.4	6295.3	7269.7
FJ478630.1	569356	7791.0	7188.6	4191.5	9961.9	11973.2	11738.4
GQ979958.1	532793	1691.2	1485.6	8662.5	6843.3	2136.4	2317.6
AB166882.1	104301	4707.9	3690.4	4806.2	4065.0	3169.4	4707.6
GU454933.1	520944	4340.4	7203.0	6062.8	3442.5	3224.6	3761.4
AB192066.1	143225	82.0	171.3	207.1	124.1	130.6	156.2
GQ065924.1	397799	641.2	1026.4	2264.6	1652.7	949.0	955.1
GU454955.1	525767	8578.2	6438.1	13314.6	8695.4	5969.6	5582.7
DQ517100.1	160794	165.4	392.4	391.8	776.0	112.6	68.2
GU222238.1	586616	2299.4	3411.5	4770.0	3193.7	1898.3	2351.9
AY770497.1	143561	3194.3	5336.2	2973.3	3532.3	3631.2	3278.6
AB486739.1	585587	1850.8	2765.1	3377.7	1437.3	1283.8	1663.0
GQ231337.1	560504	1223.0	1953.8	1811.6	1688.7	3117.9	5238.6
AF011343.1	6783	6053.6	7580.4	11904.9	9789.7	4374.7	8275.2
FJ823940.1	529251	5176.2	6745.8	8497.9	10441.1	7843.7	6197.9
AY662036.1	136814	2609.3	2562.2	8187.6	7439.7	3498.8	4427.1
FJ479338.1	539491	6160.2	6018.0	5985.0	7532.9	4803.2	5963.6
GQ108087.1	430940	7636.0	6902.8	13579.7	8910.6	7322.7	8856.1
EU244087.1	360080	9110.9	8992.1	7845.6	8999.9	12127.7	10333.5
EF019494.1	214657	5170.0	4155.1	4706.7	3839.4	5228.6	5242.2
AB049763.1	27927	60.8	46.3	99.2	117.5	219.2	29.4

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s__Zoogloea ramigera	16905

DQ665916.1 gg_id:168182 Garrityella koreensis str. 5YN10-9
AF047462.1 gg_id:6696 Dechloromonas agitata str. CKB
GQ389180.1 gg_id:576785 quality deterioration drinking system during serious red water outbreak clone D50
GQ092099.1 gg_id:399670 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw406a11c
EU104068.1 gg_id:321632 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU639302.1 gg_id:355190 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AM268352.1 gg_id:186954 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
GQ102268.1 gg_id:399299 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ074891.1 gg_id:413877 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ104713.1 gg_id:418639 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ083179.1 gg_id:447534 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU639164.1 gg_id:316640 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AB201043.1 gg_id:154231 Zoogloea oryzae str. -7
GQ104097.1 gg_id:424182 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw563b0
GQ093001.1 gg_id:451554 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407g11c
GQ103863.1 gg_id:381601 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AM268341.1 gg_id:194016 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
EU834782.1 gg_id:591111 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se
AY689093.1 gg_id:103490 activated sludge clone KRZ70
GQ099610.1 gg_id:377523 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
GQ084706.1 gg_id:446882 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26
EU639134.1 gg_id:305091 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
GQ098121.1 gg_id:414445 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ104481.1 gg_id:381484 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ375501.1 gg_id:540537 T-RFLP powerful tool rapid assessment cells microbial fuel cell sheet carbon paper an
GQ102905.1 gg_id:421705 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ096102.1 gg_id:437453 Topographical and Temporal Human Skin Microbiome skin back clone nbw386f04c1
GQ083393.1 gg_id:443756 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ106855.1 gg_id:431721 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw541g0
GQ106511.1 gg_id:409008 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ096575.1 gg_id:407705 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw389h0
GQ092008.1 gg_id:423840 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw405a04c
GQ092845.1 gg_id:380337 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
AF502233.1 gg_id:59335 EBPR sludge lab scale clone HP1A03
GQ106704.1 gg_id:422891 Topographical and Temporal Human Skin Microbiome skin back clone nbw539e12c1
GQ092947.1 gg_id:439576 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407b05c
GQ105471.1 gg_id:430660 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ096373.1 gg_id:385515 Topographical and Temporal Human Skin Microbiome skin back clone nbw387d08c1
GQ095282.1 gg_id:374709 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
CU466885.1 gg_id:344216 Evry wastewater treatment plant anoxic basin clone
D14254.1 gg_id:6731 Zoogloea ramigera str. IAM12136

DQ665916.1	168182	1023.3	883.8	2974.1	2674.4	777.7	957.2
AF047462.1	6696	1268.8	532.8	2244.3	2647.2	840.1	1058.4
GQ389180.1	576785	7996.0	5270.3	18414.6	11267.2	5423.8	5153.4
GQ092099.1	399670	3764.5	2997.2	6784.1	4206.0	5269.4	7383.7
EU104068.1	321632	6991.3	5947.0	8467.5	9553.5	8135.1	6024.9
EU639302.1	355190	2460.9	2034.6	4421.0	2650.1	977.2	1549.5
AM268352.1	186954	4910.7	4564.8	7654.8	5049.7	6240.7	4641.4
GQ102268.1	399299	7171.1	5676.5	9408.0	6883.8	4677.7	5781.4
GQ074891.1	413877	16151.5	16630.9	17610.5	13129.2	16532.8	15679.7
GQ104713.1	418639	13011.7	11401.2	16040.7	14288.8	13576.5	11087.1
GQ083179.1	447534	11002.6	8836.9	6349.6	11084.2	14236.6	11414.5
EU639164.1	316640	2717.7	1924.4	3081.7	3210.4	1551.5	1860.3
AB201043.1	154231	4900.9	3896.5	8706.6	6477.2	3511.4	4885.5
GQ104097.1	424182	14892.8	13187.9	18235.4	13882.4	15418.9	14215.7
GQ093001.1	451554	11188.8	5345.3	13184.5	7950.4	6841.8	5102.2
GQ103863.1	381601	5366.5	5983.1	8634.2	4802.7	7792.4	6183.4
AM268341.1	194016	7667.4	6655.1	12310.9	11539.6	7380.6	8595.8
EU834782.1	591111	2961.3	2351.1	4791.6	2662.9	2636.5	2277.4
AY689093.1	103490	9661.4	10359.6	15444.7	9612.5	15554.5	11440.5
GQ099610.1	377523	5584.8	4534.4	9471.8	6833.1	11269.3	6215.1
GQ084706.1	446882	10274.3	7895.5	12223.2	10434.3	9051.6	8258.8
EU639134.1	305091	3285.7	3455.5	7069.4	4944.0	4758.2	7562.4
GQ098121.1	414445	20546.6	22247.4	24155.1	17147.0	24130.3	20057.9
GQ104481.1	381484	6871.7	6686.0	10907.8	9277.2	11678.3	7796.7
FJ375501.1	540537	81.4	1165.3	698.1	245.3	134.4	118.2
GQ102905.1	421705	6299.9	5609.1	9737.7	6243.5	5932.3	5171.9
GQ096102.1	437453	4870.3	4055.0	8255.7	5509.9	6281.9	6655.0
GQ083393.1	443756	9759.8	9428.8	14270.8	9575.7	12768.3	10478.5
GQ106855.1	431721	5325.6	4272.4	9281.6	5377.3	6283.3	5158.6
GQ106511.1	409008	15045.9	14391.7	17045.1	12495.9	15354.5	14946.2
GQ096575.1	407705	8290.7	4959.8	11828.2	8324.0	6689.8	6593.8
GQ092008.1	423840	7348.3	7570.5	12923.7	6166.4	8465.7	7212.9
GQ092845.1	380337	337.2	273.7	1483.0	1224.1	5949.4	1498.9
AF502233.1	59335	5606.8	4032.0	7614.9	10007.4	3034.8	2977.3
GQ106704.1	422891	5595.8	5467.4	9405.4	3984.3	6069.8	5006.6
GQ092947.1	439576	18238.7	17667.7	15011.7	13521.7	18934.9	15849.0
GQ105471.1	430660	6544.8	2909.7	5500.4	5378.0	6144.7	6190.1
GQ096373.1	385515	16261.1	13953.0	23650.6	15858.6	15116.6	14238.9
GQ095282.1	374709	6690.4	3004.0	10642.7	6863.6	2955.4	3558.9
CU466885.1	344216	9469.4	10118.6	12699.2	7873.3	12511.9	9500.0
D14254.1	6731	6563.6	4515.1	8110.8	7966.3	3922.1	4793.7

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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria

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g__Zoogloea
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s__Zoogloea ramigera	17402
s__Zoogloea resiniphila	16109
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AM268353.1 gg_id:174268 Functional Redundancy Versatility Rhodocyclales Activated Sludge: Improvement ar
AJ505851.1 gg_id:70483 Zoogloea resiniphila str. PIV-3A2w = DSM 14766
EF632935.1 gg_id:253630 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
EU133805.1 gg_id:249736 tallgrass prarie soil clone FFCH7204
EF020008.1 gg_id:206405 aspen rhizosphere clone Elev_16S_1398
EU589266.1 gg_id:266605 China Ningxia rice paddy field soil clone 1_E8
FJ748781.1 gg_id:567553 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar
EU276554.1 gg_id:361100 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
DQ499310.1 gg_id:159574 acidic cave snottite biofilm clone CV71
FJ810598.1 gg_id:394416 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
EF032745.1 gg_id:187854 cyanobacterial mat in lava cave clone HAVOmat01
EF018556.1 gg_id:215521 aspen rhizosphere clone Amb_16S_819
DQ351927.1 gg_id:165444 manganese oxidation soil clone JH-GY05
EU287309.1 gg_id:254959 Pacific arctic surface sediment clone S26-9
EU133892.1 gg_id:243583 tallgrass prarie soil clone FFCH4041
FJ535105.1 gg_id:534686 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM119
AB294327.1 gg_id:204721 Microbial structure deep coal seem groundwater stream clone SWB16
GQ302538.1 gg_id:536176 prokaryotic sediment Shawan methods cold spring clone sw-xj248
DQ413098.1 gg_id:153104 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
DQ228413.1 gg_id:144006 microbial compositions two subglacial possible role microbes chemical weathering p
AF280846.1 gg_id:17553 bioreactor clone mle1-7
AB179499.1 gg_id:100324 sedimentary rock clone MIZ08
GQ262859.1 gg_id:585913 Structure Simulated Level Waste Site simulated level waste site clone F1_34X
EU133840.1 gg_id:253509 tallgrass prarie soil clone FFCH1549
AJ581593.1 gg_id:93464 soil near uranium mill tailings clone KCM-B-81
DQ906845.1 gg_id:242049 Oman subsurface soil clone 10A-2
AM990454.1 gg_id:278532 Sterolibacterium sp. str. TKU1
AM935260.1 gg_id:543221 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ261308.1 gg_id:552362 Study on Sediment sediment Dongping Lake clone 1S2-21
GQ263997.1 gg_id:509604 Structure Simulated Level Waste Site simulated level waste site clone WC2_91
AY555807.1 gg_id:102883 Bor Khlueng hot spring clone PK332
EF516193.1 gg_id:219982 grassland soil clone FCPS563
NR_024834.1 gg_id:573240 Thiobacter subterraneus str. C55; JCM 12421
DQ413075.1 gg_id:150728 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
GQ263936.1 gg_id:593889 Structure Simulated Level Waste Site simulated level waste site clone WC2_188
DQ906784.1 gg_id:251160 Oman subsurface soil clone 2B-6
EF540388.1 gg_id:225930 oil-shale semi-coke solid waste clone MJK28
EF018248.1 gg_id:214289 aspen rhizosphere clone Amb_16S_603
GQ302536.1 gg_id:560421 prokaryotic sediment Shawan methods cold spring clone sw-xj169
EF019282.1 gg_id:206997 aspen rhizosphere clone Elev_16S_468
FJ478674.1 gg_id:510039 species richness estimates obtained nearly and simulated pyrosequencing-generated

AM268353.1	174268	14989.0	14755.4	10638.2	11851.7	14201.3	14595.1
AJ505851.1	70483	1546.3	3086.1	8512.8	3549.1	1945.7	3567.3
EF632935.1	253630	4045.6	4224.2	8177.4	6379.9	3028.9	5052.7
EU133805.1	249736	402.8	686.0	539.1	358.4	1627.0	613.4
EF020008.1	206405	93.3	291.4	2214.9	128.0	119.1	169.4
EU589266.1	266605	6872.2	5889.8	6188.2	9320.1	7564.0	7004.3
FJ748781.1	567553	2052.8	2900.9	4069.0	3855.6	2546.4	3074.3
EU276554.1	361100	3249.2	3463.3	7571.8	6653.1	2394.2	3009.0
DQ499310.1	159574	1251.5	2586.0	4529.7	2382.6	2839.6	3125.9
FJ810598.1	394416	1552.5	1608.8	5241.9	2187.0	2800.7	3379.0
EF032745.1	187854	275.1	253.9	380.5	222.7	213.8	264.0
EF018556.1	215521	44.7	99.0	486.8	106.3	3679.3	1614.1
DQ351927.1	165444	8703.7	8596.9	10978.6	12936.5	9151.8	8213.4
EU287309.1	254959	1948.1	2743.2	4493.4	3367.8	3151.6	4109.3
EU133892.1	243583	6878.0	9330.0	10607.1	7872.6	11483.4	9393.8
FJ535105.1	534686	7778.3	8292.0	13660.8	8366.6	10251.7	8566.8
AB294327.1	204721	3112.4	6530.3	10618.6	6074.4	9344.3	9616.1
GQ302538.1	536176	6201.5	5145.1	7973.9	9448.6	4346.4	7722.0
DQ413098.1	153104	2346.8	2269.5	2156.0	2978.7	4845.0	4096.9
DQ228413.1	144006	359.4	372.8	1986.4	1244.2	488.4	650.6
AF280846.1	17553	6212.8	6855.5	5828.4	6771.4	7541.0	4712.3
AB179499.1	100324	2579.7	2541.4	4726.2	4264.9	4065.9	3252.3
GQ262859.1	585913	6439.6	4538.3	10449.0	8776.2	5418.5	6585.3
EU133840.1	253509	2630.7	3362.7	3907.8	1829.5	5841.9	5024.6
AJ581593.1	93464	9163.1	8672.6	9994.7	11636.5	11843.4	11413.2
DQ906845.1	242049	10764.6	13827.2	10419.2	10820.6	14914.7	15364.4
AM990454.1	278532	4161.5	4747.4	4279.3	3717.1	8591.1	6068.0
AM935260.1	543221	4960.6	4528.9	8918.6	6153.0	5075.3	5892.1
GQ261308.1	552362	6890.0	5834.4	10540.0	7443.0	9330.6	8666.0
GQ263997.1	509604	4774.4	6167.3	3574.5	2943.4	6628.2	6523.9
AY555807.1	102883	57.7	159.6	628.6	97.3	98.7	126.5
EF516193.1	219982	48.9	76.6	227.1	128.4	90.3	114.2
NR_024834.1	573240	260.9	226.6	150.0	1812.3	232.1	227.5
DQ413075.1	150728	4808.0	5053.0	5858.0	4741.0	7170.8	5466.0
GQ263936.1	593889	6009.5	6985.2	13248.5	9307.1	9293.8	8959.4
DQ906784.1	251160	8768.1	9389.7	3918.9	5466.0	6487.3	8022.5
EF540388.1	225930	463.8	538.9	1587.4	565.9	283.1	617.4
EF018248.1	214289	6248.5	8126.1	7150.5	5840.8	8826.1	8103.5
GQ302536.1	560421	118.2	493.7	3747.9	376.4	1065.5	546.2
EF019282.1	206997	477.8	455.2	1429.5	1987.8	336.2	961.7
FJ478674.1	510039	8451.7	9936.1	8990.1	10794.1	7782.9	8523.9

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EU881149.1 gg_id:352105 Karst region primary forest soil clone KPF200711-158
EU335200.1 gg_id:249281 Changes microbial metabolic and along hydrogeochemically variable profile saturate
GQ263985.1 gg_id:545926 Structure Simulated Level Waste Site simulated level waste site clone WC2_75
GQ302534.1 gg_id:540962 prokaryotic sediment Shawan methods cold spring clone sw-xj69
DQ413095.1 gg_id:152559 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
DQ499286.1 gg_id:159638 acidic cave snottite biofilm clone CV30
GQ263251.1 gg_id:585912 Structure Simulated Level Waste Site simulated level waste site clone F3_77X2
DQ823210.1 gg_id:171073 Techniques Microbial Studies Oregon Caves National Monument Quad 17 on trail cl
EF019065.1 gg_id:214169 aspen rhizosphere clone Amb_16S_1641
FJ517093.1 gg_id:510574 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
EU133787.1 gg_id:257306 tallgrass prarie soil clone FFCH5275
EU449747.1 gg_id:575467 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
GQ262854.1 gg_id:593141 Structure Simulated Level Waste Site simulated level waste site clone F1_31X
GU208422.1 gg_id:588520 Study on Sediment Dongping Lake sediment clone Fh3-20
AY212696.1 gg_id:106348 water 10 m downstream manure clone 248ds10
DQ009366.1 gg_id:117907 bacterioplankton clone SPOTSAPR01_5m110
EF019806.1 gg_id:205805 aspen rhizosphere clone Elev_16S_997
AJ536880.1 gg_id:78574 uranium mining waste pile soil sample clone JG30-KF-AS41
EF516474.1 gg_id:220381 grassland soil clone FCPO565
EU440652.1 gg_id:552054 Soil are Changed Agricultural Practices agricultural soil clone Plot17-F06
AY050578.1 gg_id:71612 MCB-contaminated groundwater-treating reactor clone GOUTA6
EF492893.1 gg_id:243674 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EU753671.1 gg_id:341483 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite
AJ519655.1 gg_id:76131 uranium mill tailings soil sample clone GuBH2-AD-29 proteobacterium
AJ518781.1 gg_id:75238 uranium mining waste pile clone JG37-AG-7 proteobacterium
EU133774.1 gg_id:244282 tallgrass prarie soil clone FFCH3050
DQ837228.1 gg_id:248208 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_42
EU133778.1 gg_id:246758 tallgrass prarie soil clone FFCH17581
AY922034.1 gg_id:114213 farm soil clone AKYG576
EF562187.1 gg_id:257648 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
DQ499281.1 gg_id:159652 acidic cave snottite biofilm clone CV21
FJ716013.1 gg_id:558969 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina
EF516456.1 gg_id:222917 grassland soil clone FCPS389
AB179533.1 gg_id:101884 sedimentary rock clone MIZ42
DQ451461.1 gg_id:156973 forest soil clone FAC22
GQ396825.1 gg_id:557255 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EF019880.1 gg_id:204943 aspen rhizosphere clone Elev_16S_1242
DQ404836.1 gg_id:154858 contaminated sediment clone 655965
EU445220.1 gg_id:555446 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R48
AY922053.1 gg_id:113596 farm soil clone AKYG676
DQ640725.1 gg_id:230327 full-scale EBPR sludge clone Skagen120

EU881149.1	352105	3886.5	4246.3	8233.9	6748.8	4165.7	4412.5
EU335200.1	249281	10343.6	7395.5	12503.7	12548.1	5782.2	9724.1
GQ263985.1	545926	4961.5	4898.2	8240.0	9533.0	3927.6	4568.0
GQ302534.1	540962	3198.9	3983.3	6649.7	7030.1	3078.8	4665.5
DQ413095.1	152559	684.1	1108.8	1974.0	2089.6	1118.3	1550.1
DQ499286.1	159638	472.9	574.2	1013.4	271.6	552.0	323.2
GQ263251.1	585912	9381.9	8868.9	5933.0	10952.0	11038.5	10343.5
DQ823210.1	171073	5806.5	7272.5	5753.0	5386.8	8137.4	6631.3
EF019065.1	214169	78.1	33.4	63.2	146.2	69.8	39.8
FJ517093.1	510574	517.0	550.2	831.3	2135.5	3710.3	5745.1
EU133787.1	257306	623.2	1485.3	1735.6	1836.5	4009.9	5502.3
EU449747.1	575467	211.7	228.9	1280.9	287.5	177.9	143.0
GQ262854.1	593141	13396.2	11840.8	10637.7	11409.4	11263.2	12268.6
GU208422.1	588520	1921.9	3180.9	5064.2	3066.6	7049.0	5642.9
AY212696.1	106348	10076.8	7679.4	10687.4	11289.2	8435.3	11012.3
DQ009366.1	117907	23.6	37.4	33.7	94.2	62.9	31.7
EF019806.1	205805	7141.4	7615.2	8018.5	7663.2	8658.9	9442.6
AJ536880.1	78574	4422.7	3950.5	12835.0	6556.2	2335.6	4594.3
EF516474.1	220381	8718.8	9675.0	8706.4	6826.0	5863.7	7202.4
EU440652.1	552054	5183.1	5320.5	4241.9	7272.2	2609.0	4856.2
AY050578.1	71612	6454.1	5135.5	11052.9	11757.0	4382.4	6083.0
EF492893.1	243674	3749.8	4188.9	4338.5	5390.8	6242.9	5746.7
EU753671.1	341483	4205.6	4000.8	8311.3	4559.7	2684.6	3780.7
AJ519655.1	76131	2792.4	2270.5	12871.7	5815.1	2385.6	2392.2
AJ518781.1	75238	3307.7	3714.7	5373.3	5250.6	4314.3	4116.6
EU133774.1	244282	2511.0	1743.5	4038.3	3969.4	2944.3	3570.9
DQ837228.1	248208	3725.3	2366.6	2991.1	4388.6	2181.0	3795.1
EU133778.1	246758	2919.6	4368.1	4682.1	2140.3	1990.9	4234.7
AY922034.1	114213	5446.8	3693.2	8566.9	7171.1	3381.6	4445.3
EF562187.1	257648	2972.0	3560.9	5372.6	3350.5	5818.2	3629.8
DQ499281.1	159652	5077.8	4393.1	6171.3	8713.4	3409.6	6705.4
FJ716013.1	558969	3108.9	4266.4	7563.1	3630.5	2663.6	3549.6
EF516456.1	222917	3628.4	4842.6	6984.7	6078.2	3562.1	8032.7
AB179533.1	101884	488.0	726.6	2330.0	1005.2	151.0	196.9
DQ451461.1	156973	33.6	65.8	450.7	111.8	96.5	178.3
GQ396825.1	557255	2002.9	1887.6	3042.8	3696.9	1799.2	3259.9
EF019880.1	204943	3566.8	4966.6	4008.7	3128.7	3307.1	3413.9
DQ404836.1	154858	2529.2	2278.2	7763.9	2954.5	2007.2	2599.7
EU445220.1	555446	4009.1	1349.3	5077.9	4326.0	1474.0	2914.6
AY922053.1	113596	6617.8	5235.7	5762.6	8619.7	2240.8	4443.6
DQ640725.1	230327	5081.7	5303.3	14583.9	8355.5	7147.2	4224.3

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AB486689.1 gg_id:580170 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
FJ810580.1 gg_id:375861 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
AY328747.1 gg_id:90051 drinking water system simulator clone DSSD49
EF492933.1 gg_id:257753 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AB294323.1 gg_id:210077 Microbial structure deep coal seem groundwater stream clone SWB12
EF492932.1 gg_id:247931 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
DQ337089.1 gg_id:150172 subsurface water clone EV818SWSAP66
DQ404884.1 gg_id:155647 contaminated sediment clone 654956
AM935609.1 gg_id:561445 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB294324.1 gg_id:203879 Microbial structure deep coal seem groundwater stream clone SWB13
AY922035.1 gg_id:113557 farm soil clone AKYG578
DQ837224.1 gg_id:242598 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_8
EF540408.1 gg_id:226082 oil-shale semi-coke solid waste clone 1_24MK
EU133831.1 gg_id:241569 tallgrass prarie soil clone FFCH14189
DQ066965.1 gg_id:136009 Lake Washington sediment clone pLW-9
DQ404609.1 gg_id:150775 contaminated sediment clone 656053
EU133881.1 gg_id:256389 tallgrass prarie soil clone FFCH2157
EF019243.1 gg_id:205571 aspen rhizosphere clone Elev_16S_420
AY921920.1 gg_id:114079 farm soil clone AKYH951
FJ466376.1 gg_id:567333 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF019405.1 gg_id:216696 aspen rhizosphere clone Elev_16S_641
AY221066.1 gg_id:86386 Mammoth cave clone CCM6a
FJ810590.1 gg_id:419579 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
EF999347.1 gg_id:240278 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm
EU133877.1 gg_id:237992 tallgrass prarie soil clone FFCH1801
EF574185.1 gg_id:230954 site S25 near Coco's Island marine clone S25_529
AY907807.1 gg_id:136986 identification picoplankton contrasting waters Arabian Sea water clone A714022
EU477832.1 gg_id:267229 and validation prototype -based taxonomic microarray members genus Burkholderia
AY234747.1 gg_id:112317 soil isolate Ellin6095
EU133863.1 gg_id:249993 tallgrass prarie soil clone FFCH8270
EF516320.1 gg_id:223302 grassland soil clone FCPS762
EF516424.1 gg_id:227269 grassland soil clone FCPU607
EU881164.1 gg_id:352281 Karst region primary forest soil clone KPF200711-070
EF516735.1 gg_id:219174 grassland soil clone FCPU655
EF516835.1 gg_id:225073 grassland soil clone FCPS400
EF019212.1 gg_id:209746 aspen rhizosphere clone Amb_16S_1908
EF654711.1 gg_id:245246 suspended sludge anammox reactor clone KIST-JJY042
FJ479088.1 gg_id:555896 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ413068.1 gg_id:152782 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EF020095.1 gg_id:208009 aspen rhizosphere clone Elev_16S_1505
DQ297977.1 gg_id:142009 Microbial hydrocarbon contaminated soil clone UA5

AB486689.1	580170	6948.8	5920.3	6493.2	10571.9	7254.4	7204.0
FJ810580.1	375861	7243.4	6366.6	11897.1	5836.2	10780.5	6400.3
AY328747.1	90051	8502.5	9568.8	5513.0	8603.0	10103.7	9448.0
EF492933.1	257753	4161.3	4187.0	5075.8	5142.4	4717.7	3684.4
AB294323.1	210077	2977.6	2417.9	3909.4	3904.9	891.1	1888.6
EF492932.1	247931	2588.0	779.6	3807.1	3525.0	732.5	2075.2
DQ337089.1	150172	4871.6	5901.6	8874.9	5605.0	6548.1	5885.2
DQ404884.1	155647	5826.6	5325.3	5867.4	7675.9	4668.5	6571.3
AM935609.1	561445	6653.0	6308.4	11827.1	6445.7	4831.5	7449.9
AB294324.1	203879	3160.9	3626.1	4789.8	6226.4	5365.6	6407.3
AY922035.1	113557	16311.2	13419.0	11794.5	18230.4	14472.1	12612.5
DQ837224.1	242598	5912.7	5425.8	3826.0	4228.2	5414.8	5796.1
EF540408.1	226082	2019.1	2202.5	2715.0	2091.3	1143.5	1782.6
EU133831.1	241569	4066.5	5341.2	6017.1	5308.5	2216.6	3533.1
DQ066965.1	136009	464.2	811.9	3865.9	1633.7	1035.4	1738.7
DQ404609.1	150775	2995.2	3511.4	8098.3	3971.3	3746.3	4053.8
EU133881.1	256389	2728.0	3075.0	2600.3	3912.0	2729.2	2839.3
EF019243.1	205571	514.7	968.1	4647.3	1264.3	3186.6	1402.6
AY921920.1	114079	1339.1	1831.9	915.4	989.9	506.3	463.8
FJ466376.1	567333	10043.3	8351.7	10663.2	11087.0	14051.6	12507.0
EF019405.1	216696	903.9	1471.3	2442.1	1585.0	932.4	2281.8
AY221066.1	86386	947.1	1023.4	1065.0	874.3	1178.6	903.5
FJ810590.1	419579	4150.7	4700.8	7778.4	10028.6	3337.1	5476.2
EF999347.1	240278	3597.9	3302.2	5164.1	3945.3	1726.6	1927.4
EU133877.1	237992	3625.2	3074.9	9616.4	3789.6	2084.9	3140.7
EF574185.1	230954	4000.4	4664.7	6381.2	6270.9	5360.0	4457.3
AY907807.1	136986	1493.6	1928.1	2920.4	1749.1	5194.3	3737.2
EU477832.1	267229	4548.8	3385.5	5652.7	5536.0	2845.4	3790.1
AY234747.1	112317	724.0	1808.7	1234.1	783.5	508.9	630.6
EU133863.1	249993	3460.0	3987.5	6879.2	4141.6	2912.9	3887.2
EF516320.1	223302	2197.7	5035.5	5997.3	2994.8	2506.2	3370.0
EF516424.1	227269	232.3	682.0	424.4	113.2	192.4	230.0
EU881164.1	352281	7884.0	6755.4	9734.2	8991.9	7242.1	8749.9
EF516735.1	219174	2040.7	2429.5	3029.2	2551.9	469.5	503.4
EF516835.1	225073	373.8	585.9	533.3	1526.5	576.5	569.6
EF019212.1	209746	111.2	1282.9	919.9	59.9	51.7	32.0
EF654711.1	245246	493.0	1892.5	2035.1	1044.0	289.0	624.7
FJ479088.1	555896	3737.7	3723.1	8146.6	4667.8	3866.3	4779.3
DQ413068.1	152782	7662.6	7041.6	3531.6	9042.5	10700.5	9008.8
EF020095.1	208009	34.0	69.9	63.1	53.7	43.5	19.8
DQ297977.1	142009	79.4	226.0	59.3	107.5	61.8	21.6

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EF019673.1 gg_id:214047 aspen rhizosphere clone Elev_16S_829
EF516867.1 gg_id:226979 grassland soil clone FCPO570
EF516029.1 gg_id:225920 grassland soil clone FCPS638
EF019461.1 gg_id:215044 aspen rhizosphere clone Elev_16S_718
EF018914.1 gg_id:203679 aspen rhizosphere clone Amb_16S_1415
EU669638.1 gg_id:307844 soil clone S8-40
EF516006.1 gg_id:226748 grassland soil clone FCPT739
AY921954.1 gg_id:113273 farm soil clone AKYG1130
EF632895.1 gg_id:235519 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
EF516769.1 gg_id:224647 grassland soil clone FCPS759
AB294328.1 gg_id:207655 Microbial structure deep coal seem groundwater stream clone SWB17
EF516759.1 gg_id:222745 grassland soil clone FCPT632
AJ421933.2 gg_id:32837 Germany:Elbe River clone Elb205
DQ413138.1 gg_id:155225 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EU193045.1 gg_id:359069 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AB426185.1 gg_id:273001 -situ identification study benzene-degrading s under methanogenic condition anaerc
EF516394.1 gg_id:223219 grassland soil clone FCPP685
EU528239.1 gg_id:281246 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
EF516152.1 gg_id:217704 grassland soil clone FCPS619
EU223955.1 gg_id:236215 -RFLP microbes Qinghai-Tin rail soil clone 124
EF516815.1 gg_id:223079 grassland soil clone FCPU398
AY221080.1 gg_id:84108 Mammoth cave clone CCU24
EF019895.1 gg_id:210313 aspen rhizosphere clone Elev_16S_1261
EU133850.1 gg_id:236450 tallgrass prarie soil clone FFCH16997
EF516351.1 gg_id:226263 grassland soil clone FCPT411
EF019531.1 gg_id:205301 aspen rhizosphere clone Elev_16S_1034
EU881346.1 gg_id:336201 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
AY921981.1 gg_id:113247 farm soil clone AKYG1746
EF520945.1 gg_id:221665 Stable isotope probing 15N2 noncultivated diazotrophs 30 year fal soil Caldwell field
DQ676312.1 gg_id:220761 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AB294330.1 gg_id:207373 Microbial structure deep coal seem groundwater stream clone SWB19
EF020158.1 gg_id:207982 aspen rhizosphere clone Elev_16S_1590
GQ396975.1 gg_id:553957 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
FJ466126.1 gg_id:509733 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ479428.1 gg_id:583255 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU528189.1 gg_id:285197 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
EF580984.1 gg_id:277681 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM5
EF516904.1 gg_id:218538 grassland soil clone FCPS542
FJ444750.1 gg_id:551308 Cotton Rhizosphere cotton rhizosphere clone 4y-67
EF018568.1 gg_id:211547 aspen rhizosphere clone Amb_16S_835
AY921702.1 gg_id:114209 farm soil clone AKYG1579

EF019673.1	214047	944.7	2168.6	1346.0	2065.0	1500.5	2507.1
EF516867.1	226979	228.5	884.7	1924.4	275.0	299.4	413.4
EF516029.1	225920	1502.7	2591.9	1807.7	2056.7	608.1	848.2
EF019461.1	215044	1213.1	701.5	464.2	813.8	716.0	790.1
EF018914.1	203679	8853.7	8655.4	9157.9	8528.4	8179.9	8284.1
EU669638.1	307844	23.5	27.6	125.8	35.8	53.1	15.6
EF516006.1	226748	608.7	1760.6	1331.6	1124.8	897.1	909.6
AY921954.1	113273	2808.1	4471.1	4683.4	2793.4	2523.2	3105.8
EF632895.1	235519	1705.7	3052.6	3956.0	2131.2	1968.6	1743.1
EF516769.1	224647	4786.7	6029.8	6021.7	6386.8	6820.3	6583.9
AB294328.1	207655	1712.3	2563.3	4425.9	2090.1	1707.5	2271.0
EF516759.1	222745	209.0	455.9	771.7	246.1	601.2	583.3
AJ421933.2	32837	6464.6	6290.5	9964.2	6737.9	3610.7	5951.4
DQ413138.1	155225	161.3	1482.3	935.1	350.9	173.9	209.2
EU193045.1	359069	7497.7	7605.2	9156.8	6586.0	7009.4	7347.3
AB426185.1	273001	126.0	994.0	51.4	47.4	45.5	22.5
EF516394.1	223219	1979.3	2917.6	2924.5	1464.7	1951.7	1800.8
EU528239.1	281246	5202.8	7848.5	10168.4	6659.8	4909.6	5865.3
EF516152.1	217704	963.5	897.1	4968.0	1423.2	847.3	1416.4
EU223955.1	236215	1000.2	407.8	609.3	114.2	1227.4	381.6
EF516815.1	223079	149.8	938.3	874.1	167.2	136.5	187.2
AY221080.1	84108	1027.4	1712.9	2268.9	863.5	483.3	1756.1
EF019895.1	210313	4373.7	3479.0	5763.5	6365.8	3041.1	4584.9
EU133850.1	236450	11118.5	8604.3	13519.7	11663.9	8263.8	10363.0
EF516351.1	226263	9547.0	10393.6	4325.8	6302.3	8993.5	6977.4
EF019531.1	205301	20.7	83.3	42.0	51.8	51.6	27.3
EU881346.1	336201	2982.7	3677.4	5764.2	3048.4	2002.5	3267.2
AY921981.1	113247	1624.2	2797.3	3088.5	1537.9	631.7	522.3
EF520945.1	221665	684.4	2149.9	2397.3	1800.4	578.4	468.3
DQ676312.1	220761	7192.9	7785.0	4864.7	7979.0	10369.3	7178.8
AB294330.1	207373	40.1	133.4	267.5	80.1	74.1	43.8
EF020158.1	207982	5383.1	3445.6	11973.7	6797.3	6220.8	5652.3
GQ396975.1	553957	2261.8	1759.8	4641.1	3616.2	3647.2	6494.7
FJ466126.1	509733	4034.2	4648.5	7148.8	4815.6	2865.7	4063.7
FJ479428.1	583255	2842.1	3333.9	6960.5	4023.6	5398.2	2848.6
EU528189.1	285197	7436.3	8381.6	15541.1	9676.4	7284.3	7356.7
EF580984.1	277681	9631.3	8819.0	8793.1	8765.0	6428.9	6460.8
EF516904.1	218538	6478.0	8989.5	11058.8	6331.3	13182.9	7014.9
FJ444750.1	551308	3509.6	3119.4	5558.0	3242.3	5450.3	3717.5
EF018568.1	211547	43.1	96.1	182.0	65.7	57.5	51.7
AY921702.1	114209	4241.4	5543.0	8214.2	4603.8	5094.5	4140.6

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EF203189.1 gg_id:215199 phylotypes sediments Lake Kastoria Greece sediment clone Kas142B
EF516051.1 gg_id:224259 grassland soil clone FCPU665
EF516025.1 gg_id:218017 grassland soil clone FCPT567
GU208364.1 gg_id:576056 Study on Sediment Dongping Lake sediment clone Td4-20
EF540369.1 gg_id:220551 oil-shale semi-coke solid waste clone 09B_MJK
EF540415.1 gg_id:220324 oil-shale semi-coke solid waste clone 1_20MK
EF540371.1 gg_id:226578 oil-shale semi-coke solid waste clone 17C_MJK
EF018962.1 gg_id:215229 aspen rhizosphere clone Amb_16S_1476
AB488102.1 gg_id:551424 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
EU404008.1 gg_id:355651 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
EF516891.1 gg_id:222729 grassland soil clone FCPP448
AM935489.1 gg_id:548533 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF590004.2 gg_id:234053 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
EF516321.1 gg_id:220011 grassland soil clone FCPN390
AB286353.1 gg_id:204179 Reducing production and domination comamonadaceae reducing oxygen supply was
AB286450.1 gg_id:205044 Reducing production and domination comamonadaceae reducing oxygen supply was
DQ310741.1 gg_id:200807 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC(
EF516268.1 gg_id:224900 grassland soil clone FCPP617
GQ396994.1 gg_id:593511 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EF580928.1 gg_id:278471 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1:
EU340157.1 gg_id:238343 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
EU340165.1 gg_id:237526 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
EU104188.1 gg_id:341168 Evidence Comamonadaceae determinants settling performance activated sludge clo
CU924494.1 gg_id:561226 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AF371865.1 gg_id:25562 swine intestine clone p-2552-9F5
EU459462.1 gg_id:296722 capybara feces clone CAP_aah97f02
EU459519.1 gg_id:294489 capybara feces clone CAP_aah99a09
FJ535157.1 gg_id:574522 Contamination risk vegetables Arcobacter during post-harvest processing water carrc
AF418961.1 gg_id:38016 USA: Colorado Fort collins Horsetooth Reservoir clone HTG2
EU778115.1 gg_id:356250 feces clone RL388_aao93c10
EF620467.1 gg_id:257876 Ralstonia sp. str. ISSDS-784
EU978820.1 gg_id:536916 and metabolic potential metagenome glacier ice clone glb332c
EF590017.2 gg_id:228077 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
DQ631725.1 gg_id:245791 sp. OC32
EU443934.1 gg_id:268574 sp. str. o6-5b
EU652615.1 gg_id:277698 Seasonal variation microbial Yel Sea sediment clone B8S-8
EU443952.1 gg_id:263927 sp. str. s3-3
AF084862.1 gg_id:19894 Bdellovibrio sp. str. JS7
FJ203067.1 gg_id:324529 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
EU443943.1 gg_id:274526 sp. str. 2bg
EU443963.1 gg_id:269969 sp. str. w5-3

EF203189.1	215199	6781.0	4735.6	6756.5	7636.0	4030.8	3324.1
EF516051.1	224259	8396.2	9061.0	7086.2	7903.5	11133.4	7307.4
EF516025.1	218017	791.8	460.2	1047.9	1338.6	198.2	548.1
GU208364.1	576056	3461.8	3972.3	8997.0	6861.3	4725.3	3632.4
EF540369.1	220551	6498.3	7103.7	14964.4	11770.7	5345.1	6787.7
EF540415.1	220324	39.6	103.8	192.0	75.2	120.3	59.8
EF540371.1	226578	5038.0	5719.6	9332.6	6757.9	5275.1	5414.9
EF018962.1	215229	3742.2	870.3	5452.8	5395.4	575.3	1686.1
AB488102.1	551424	10368.8	9644.4	8485.7	10524.9	11378.6	10002.6
EU404008.1	355651	2320.0	1918.5	2372.0	3638.3	545.0	1174.2
EF516891.1	222729	1284.0	182.3	2244.3	3889.1	117.9	235.6
AM935489.1	548533	58.9	108.3	922.2	51.1	147.4	334.6
EF590004.2	234053	2297.5	2188.1	9115.3	7681.7	2003.9	2657.8
EF516321.1	220011	1974.7	2739.1	4376.8	1764.7	6039.0	2434.2
AB286353.1	204179	1464.4	1410.4	2975.4	2336.8	1091.5	2144.3
AB286450.1	205044	630.4	1343.4	4354.4	1533.8	4125.1	9075.7
DQ310741.1	200807	5236.5	6014.6	7871.7	8028.8	4999.8	6717.8
EF516268.1	224900	1429.5	776.5	3677.9	3417.7	865.9	505.9
GQ396994.1	593511	5798.6	6617.5	19096.8	9707.8	9983.8	7510.4
EF580928.1	278471	16121.3	15702.2	12499.0	11075.1	16644.7	14234.2
EU340157.1	238343	3576.6	2378.2	4486.5	7240.0	3750.6	3727.2
EU340165.1	237526	10995.3	11213.3	16300.0	12341.8	13442.8	11018.0
EU104188.1	341168	754.9	1125.5	2363.6	1456.1	2122.8	1500.0
CU924494.1	561226	16600.6	14801.2	21884.6	13313.7	17327.7	14980.1
AF371865.1	25562	1357.0	1360.1	1358.2	1227.8	3793.3	2553.9
EU459462.1	296722	5185.4	4957.8	5869.5	6614.2	4527.1	3644.5
EU459519.1	294489	4472.3	3282.5	3527.5	4962.7	3200.4	5729.8
FJ535157.1	574522	2073.6	1321.0	2572.8	5649.2	966.1	2316.9
AF418961.1	38016	2145.1	1673.0	1523.1	3533.2	1505.9	1356.6
EU778115.1	356250	204.7	488.1	529.4	381.2	256.7	363.3
EF620467.1	257876	1863.7	2460.0	4884.1	2864.0	1404.5	1606.5
EU978820.1	536916	2693.3	2457.4	3417.2	3951.9	883.6	1868.1
EF590017.2	228077	3804.1	1972.0	8549.5	5952.4	628.2	1957.8
DQ631725.1	245791	22.0	33.3	23.6	51.6	51.6	21.8
EU443934.1	268574	5163.0	5230.1	7777.7	4939.4	5614.0	4667.4
EU652615.1	277698	5663.5	6730.0	3868.4	3736.5	4388.8	4117.3
EU443952.1	263927	11.7	33.0	41.0	51.9	51.8	22.8
AF084862.1	19894	1479.1	1827.9	3266.2	2000.7	2458.3	3454.3
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EU443943.1	274526	5960.8	5557.2	5021.1	6542.5	6332.1	5383.1
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AF084854.1 gg_id:106487 marinus str. SJ
EU443935.1 gg_id:258583 sp. str. b6-10b
EF092436.2 gg_id:198558 sp. NB2
DQ631776.1 gg_id:246590 sp. NZ7
EF188429.1 gg_id:346586 Microbial Altamira Cave clone 236
AY947967.1 gg_id:141636 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
AJ288899.1 gg_id:49685 stolpii str. DSM 12778
EU805174.1 gg_id:311266 It's all ranking aquatic 250 miles Panama City clone 6C233166
EU662557.1 gg_id:580005 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
EU237338.1 gg_id:239851 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as
DQ266898.1 gg_id:141116 Cloning and microorganism genes alkaline soil clone pGXAR13
EF687517.1 gg_id:281539 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
AB369189.1 gg_id:239066 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
AY294221.1 gg_id:101065 sp. str. PNEc1
EU101250.1 gg_id:254683 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
GU119471.1 gg_id:564132 Threatened Corals Provide Microbial Habitats reef water clone Reef_F14
AB176175.1 gg_id:182905 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
AJ278146.1 gg_id:22594 Bdellovibrio sp. str. SD1 sewage
EF574402.1 gg_id:229914 site S25 near Coco's Island marine clone S25_746
GQ351210.1 gg_id:590861 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
DQ676387.1 gg_id:218005 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
DQ133926.1 gg_id:168155 Dominant microbial biofilms frasassi cave system Italy limestone-corroding stream b
AJ290009.1 gg_id:40173 Germany: Lake Fuchskuhle north basin clone FukuN9 FukuN9
GU369899.1 gg_id:518456 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
AJ292518.1 gg_id:38566 Bdellovibrio sp. W str. ATCC 27047
AF148939.1 gg_id:30112 Bdellovibrio str. BRP4
EU050708.1 gg_id:247981 Microbial waters production water Daqing oil field clone DQ328-109
AJ292759.1 gg_id:40800 Bdellovibrio HD100 str. HD 100 DSM 50701
EU050700.1 gg_id:244273 Microbial waters production water Daqing oil field clone DQ328-1
DQ847445.1 gg_id:172283 human forearm skin clone GR2-101
GQ113033.1 gg_id:410201 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
DQ413094.1 gg_id:152494 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
AB286607.1 gg_id:213370 Reducing production and domination comamonadaceae reducing oxygen supply was
FJ542862.1 gg_id:525171 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
AM233527.1 gg_id:320761 Multiple symbionts two species co-occurring gutless oligochaete worms Mediterrar
CU466777.1 gg_id:338371 Evry wastewater treatment plant anoxic basin clone
EF687743.1 gg_id:243041 Bdellovibrio sp. str. JSS
GQ039893.1 gg_id:416757 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
AY294215.1 gg_id:105561 Bdellovibrio sp. str. MPA
EU104139.1 gg_id:353499 Evidence Comamonadaceae determinants settling performance activated sludge clo
DQ640659.1 gg_id:232532 full-scale EBPR sludge clone Skagenf81

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EU443935.1	258583	2131.1	4663.2	2908.1	3556.8	4892.2	4886.5
EF092436.2	198558	5357.9	4737.6	4547.0	5418.5	3513.0	2462.6
DQ631776.1	246590	1453.6	2313.2	5565.8	1593.5	1754.9	1853.4
EF188429.1	346586	772.6	1342.2	4181.4	1256.7	1211.8	2164.9
AY947967.1	141636	87.8	174.1	4662.6	615.0	61.6	25.9
AJ288899.1	49685	794.5	1174.4	7503.2	946.2	420.6	244.9
EU805174.1	311266	2856.3	4582.2	7655.8	2222.4	5113.7	3835.3
EU662557.1	580005	9683.8	10353.4	8946.3	7452.6	9978.2	8997.5
EU237338.1	239851	7405.5	7098.3	12361.0	6321.0	9381.6	9400.7
DQ266898.1	141116	1281.3	1347.3	10650.7	2631.0	715.4	741.6
EF687517.1	281539	560.7	1257.8	5220.2	1633.0	1305.4	2478.2
AB369189.1	239066	3112.5	4217.0	9743.5	3523.9	5392.5	6343.4
AY294221.1	101065	6439.0	6910.6	9652.2	3899.8	2335.5	2236.8
EU101250.1	254683	1518.0	4267.2	5475.4	3353.8	5112.1	2173.8
GU119471.1	564132	4814.8	5330.1	5369.9	3733.4	8302.2	6641.0
AB176175.1	182905	339.4	620.0	976.2	358.6	307.1	664.3
AJ278146.1	22594	191.1	1268.7	5724.6	1536.6	249.9	201.4
EF574402.1	229914	283.5	140.5	952.0	279.2	112.2	253.9
GQ351210.1	590861	2805.8	3103.6	4663.2	2421.7	2640.5	3612.2
DQ676387.1	218005	75.8	108.2	3537.9	398.7	182.0	79.2
DQ133926.1	168155	913.9	2441.2	1381.6	1271.4	694.9	2759.6
AJ290009.1	40173	633.5	944.3	9701.0	1224.0	1579.5	789.0
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AJ292518.1	38566	4528.2	5750.9	4792.5	4471.7	4158.0	3843.9
AF148939.1	30112	6991.8	5922.3	10162.8	6576.0	7744.4	6936.9
EU050708.1	247981	2890.0	4055.3	8154.9	4920.8	7919.6	4240.3
AJ292759.1	40800	1551.8	2087.0	2383.4	891.5	813.6	751.7
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DQ847445.1	172283	38.3	122.9	907.1	119.4	85.5	61.3
GQ113033.1	410201	4971.6	4383.6	4438.0	4475.5	5202.7	6256.8
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AB286607.1	213370	229.2	702.8	4904.3	481.9	605.0	714.7
FJ542862.1	525171	5560.3	5213.8	5543.4	3502.6	7457.6	5984.5
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EF687743.1	243041	3520.1	4137.1	5620.2	2072.0	10616.3	7396.7
GQ039893.1	416757	48.7	101.8	1410.1	117.8	94.9	58.1
AY294215.1	105561	2025.9	3545.6	4480.3	2270.8	1911.8	2515.1
EU104139.1	353499	89.6	198.5	1580.5	402.8	139.3	77.6
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AY177783.1 gg_id:78428 soil clone
GQ024567.1 gg_id:485103 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123h01c:
EU884926.1 gg_id:337320 Bdellovibrio sp. str. JSF2
EU937847.1 gg_id:307774 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AF148941.1 gg_id:74869 Bdellovibrio str. TRA2
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EU134532.1 gg_id:238695 tallgrass prarie soil clone FFCH17748
AY921748.1 gg_id:113368 farm soil clone AKYH800
FM253670.1 gg_id:343998 Rock gold mine unusually microbial biofilm clone G01-2
EU431666.1 gg_id:542199 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
EF516458.1 gg_id:227450 grassland soil clone FCPT629
EU134406.1 gg_id:257948 tallgrass prarie soil clone FFCH7045
EU134524.1 gg_id:256205 tallgrass prarie soil clone FFCH8734
EU134527.1 gg_id:254193 tallgrass prarie soil clone FFCH9759
EU133256.1 gg_id:247777 tallgrass prarie soil clone FFCH18766
EF018594.1 gg_id:209570 aspen rhizosphere clone Amb_16S_865
FJ542822.1 gg_id:511221 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
EU978839.1 gg_id:591758 and metabolic potential metagenome glacier ice clone glb351c
FJ425595.1 gg_id:365052 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl
FJ202533.1 gg_id:352758 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB487112.1 gg_id:562287 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EF516682.1 gg_id:224255 grassland soil clone FCPS531
DQ129144.2 gg_id:189151 forest soil clone CWT ST01_F02
EF442982.1 gg_id:239332 Desulfobacterium catecholicum str. Kette
FJ516957.1 gg_id:511303 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
U12253.1 gg_id:10829 Desulfobulbus rhabdoformis str. M16
GU304430.1 gg_id:581441 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
DQ831531.1 gg_id:162379 Activity and sulphate-reducing contrasting sediments River Colne estuary UK brackis
EU844167.1 gg_id:341591 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB189697.1 gg_id:114072 termite gut homogenate clone Tc-66
DQ394978.1 gg_id:151814 harbor sediment clone VHS-B4-9
AY548789.1 gg_id:105497 Desulfobulbus propionicus str. DSM 2032
NR_029305.1 gg_id:590669 Desulfobulbus elongatus str. FP; DSM 2908
FJ769451.1 gg_id:542644 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana
AJ535238.1 gg_id:77808 marine sediment above hydrate ridge clone Hyd24-21 proteobacterium
AY355297.2 gg_id:105894 epibiontic clone C11-G5
Y13672.1 gg_id:10794 Desulfocapsa sulfexigens str. SB164P1
EU662381.1 gg_id:571160 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat
AJ511275.1 gg_id:69671 Desulfocapsa sp. Cad626
FJ497574.1 gg_id:580889 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun

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AY177783.1	78428	9614.2	10401.0	7987.0	7984.5	12593.3	10650.4
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EU884926.1	337320	674.8	1716.7	2639.5	731.1	832.5	693.9
EU937847.1	307774	8384.6	10927.0	4691.7	5245.7	5235.5	3361.4
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AY662018.1	137132	3450.1	3265.8	5804.4	2918.0	2433.7	3073.1
EU134532.1	238695	12883.6	13310.2	16114.4	13856.4	11196.4	11984.4
AY921748.1	113368	3709.2	6938.7	6349.7	3432.2	7757.0	7603.7
FM253670.1	343998	4574.8	7364.1	8906.4	5624.7	7275.8	7896.2
EU431666.1	542199	6391.8	7018.2	7741.0	6776.2	5507.4	5913.7
EF516458.1	227450	2686.9	4019.4	4305.4	3372.4	2998.1	3546.3
EU134406.1	257948	2533.0	3977.2	6904.7	2117.8	2943.0	4274.1
EU134524.1	256205	2155.9	3100.8	5807.9	2833.5	2713.7	3673.4
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EU133256.1	247777	1869.3	3409.8	4906.3	1862.9	1249.3	2180.9
EF018594.1	209570	5974.7	5744.1	5800.7	7701.2	2157.1	3439.1
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AB487112.1	562287	120.0	199.6	844.8	217.2	58.6	77.6
EF516682.1	224255	6295.8	8987.3	8161.4	6724.3	6106.7	5824.8
DQ129144.2	189151	413.5	733.1	1153.7	411.9	615.4	458.1
EF442982.1	239332	59.2	105.8	1183.8	92.9	91.6	66.2
FJ516957.1	511303	452.7	1039.9	2429.5	249.9	184.5	133.4
U12253.1	10829	19.3	11.6	32.0	43.9	48.1	21.9
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DQ831531.1	162379	1140.6	2359.0	6549.3	2002.9	1793.1	2047.5
EU844167.1	341591	893.7	1548.6	4224.1	3322.9	663.6	1332.1
AB189697.1	114072	205.5	374.4	830.7	312.2	213.8	813.1
DQ394978.1	151814	26.3	32.8	31.2	61.9	511.0	24.2
AY548789.1	105497	1177.7	1073.1	3338.1	617.4	584.1	698.1
NR_029305.1	590669	678.8	841.2	2372.7	2286.7	313.4	569.3
FJ769451.1	542644	1402.4	1722.9	3150.1	3515.9	782.6	2137.6
AJ535238.1	77808	4862.6	6599.7	9233.1	6220.4	6977.3	6417.4
AY355297.2	105894	109.2	607.1	2122.4	147.8	843.8	1441.7
Y13672.1	10794	37.9	52.5	41.8	66.0	61.5	40.0
EU662381.1	571160	5484.0	5328.6	2580.1	5347.0	7630.4	6798.4
AJ511275.1	69671	1198.5	763.5	2284.3	2037.3	601.5	750.8
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EF687474.1 gg_id:281846 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
FJ901718.1 gg_id:567131 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita
DQ925886.1 gg_id:235454 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
EU101288.1 gg_id:249303 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
X95181.1 gg_id:10792 Desulfocapsa thiozymogenes str. Bra2
EU662622.1 gg_id:583279 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
EU101286.1 gg_id:250699 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
DQ521816.1 gg_id:159745 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexico
DQ676351.1 gg_id:217639 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
FJ712571.1 gg_id:531935 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EU265788.1 gg_id:264490 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc
GU118041.1 gg_id:549531 Threatened Corals Provide Microbial Habitats clone Apal_D11
GQ850564.1 gg_id:591035 bottom water northern Bering Sea clone d75
AY177802.1 gg_id:78959 Antarctic sediment clone SB4_58
GU118122.1 gg_id:557861 Threatened Corals Provide Microbial Habitats clone Apal_M04
AF118453.1 gg_id:10810 Desulforhopalus singaporensis str. S'pore T1
GU118039.1 gg_id:581136 Threatened Corals Provide Microbial Habitats clone Apal_N04
NC_006138.1 gg_id:128538 Desulfotalea psychrophila str. LSv54
FJ664813.1 gg_id:568793 Quantitative dynamics cells plankton-fed microbial fuel cell clone PFC_6_peak_F10
AY770713.1 gg_id:110727 sea urchin Paracentrotus lividus clone PlS93
NR_024949.1 gg_id:534504 Desulfotalea arctica str. LSv514; DSM 12342
AY770715.1 gg_id:110001 sea urchin Paracentrotus lividus clone PlS95
GQ357011.1 gg_id:583377 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeLive
DQ831548.1 gg_id:170756 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
FJ203002.1 gg_id:319044 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AY177796.1 gg_id:78728 Antarctic sediment clone SB1_68
AM774321.2 gg_id:245906 Cultivation and situ quantification consistently demonstrate that two distinct group
EU617845.1 gg_id:329633 Seasonal variation microbial Yel Sea sediment clone A13S-69
AY592401.1 gg_id:103065 deep-sea mud volcano clone Amsterdam-2B-43; BC20-2B-43
FN396662.1 gg_id:550643 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V
AY327885.1 gg_id:89269 surface vent snail foot clone SF_C4-E
GU220767.1 gg_id:540615 Microbial mineralization and involved microbial Basin field temperature hydrotherm
FJ485136.1 gg_id:510228 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat
GQ246441.1 gg_id:583729 Temporal and spatial China North Yel Sea sediments clone Ld1-46
AM745146.1 gg_id:290803 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
FJ712454.1 gg_id:517813 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
DQ831544.1 gg_id:169282 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
EU981262.1 gg_id:342198 sulfate reducing living bench scale aquifer column water clone D1_SW
AF354148.1 gg_id:71200 marine methane seep clone 1431
EU981255.1 gg_id:355558 sulfate reducing living bench scale aquifer column water clone A56_SW
AB294977.1 gg_id:226332 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma

EF687474.1	281846	3023.4	2965.0	3034.1	2465.3	3089.5	2628.1
FJ901718.1	567131	545.6	1438.8	4430.8	1109.8	2094.9	2368.7
DQ925886.1	235454	9196.5	7699.2	5989.8	6854.3	12138.8	10408.7
EU101288.1	249303	148.0	158.4	699.9	85.9	52.8	130.3
X95181.1	10792	5029.0	5497.7	5719.1	6158.4	4888.0	5287.3
EU662622.1	583279	6012.9	4374.3	8427.4	5266.9	3440.6	3935.0
EU101286.1	250699	753.8	1949.8	2393.6	447.2	613.0	2905.6
DQ521816.1	159745	7861.9	7090.9	5538.2	6872.3	11029.1	9799.7
DQ676351.1	217639	8907.5	7974.1	6517.0	7378.0	7200.5	7420.9
FJ712571.1	531935	1280.6	916.8	2180.6	870.4	2539.2	1639.1
EU265788.1	264490	29.7	33.1	75.2	76.0	95.3	35.7
GU118041.1	549531	4333.9	5479.3	3949.7	4031.4	6655.4	9018.4
GQ850564.1	591035	115.1	254.8	2804.1	286.6	1767.8	152.8
AY177802.1	78959	172.2	398.7	2557.2	381.3	2882.2	658.4
GU118122.1	557861	6451.6	7289.6	9631.2	5467.1	583.8	5210.9
AF118453.1	10810	1926.1	2965.4	3969.0	839.0	692.0	986.2
GU118039.1	581136	6597.7	7467.0	5997.7	6121.5	13674.6	10923.6
NC_006138.1	128538	5281.2	6974.9	5953.4	2756.5	4982.5	4168.0
FJ664813.1	568793	213.0	2713.3	4765.3	1466.3	3923.1	2849.4
AY770713.1	110727	2429.7	3073.5	3132.3	2253.5	4328.3	3464.9
NR_024949.1	534504	518.8	591.1	1841.8	316.7	303.5	528.4
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FJ203002.1	319044	47.1	69.4	142.2	84.0	88.9	52.3
AY177796.1	78728	29.8	50.4	647.3	78.7	71.6	32.9
AM774321.2	245906	3233.8	4854.4	10467.4	3817.9	5379.1	5091.7
EU617845.1	329633	40.4	98.4	345.1	66.4	50.3	15.3
AY592401.1	103065	4231.5	3574.6	6222.6	5540.3	4387.9	5089.2
FN396662.1	550643	1611.7	2608.7	12144.4	3519.6	6573.4	3220.7
AY327885.1	89269	2902.2	2340.2	1585.3	3447.0	6527.7	5852.8
GU220767.1	540615	417.6	861.6	870.1	180.0	1209.1	460.2
FJ485136.1	510228	1595.3	2570.3	6141.4	2413.3	834.6	1082.8
GQ246441.1	583729	663.0	1168.9	1685.7	1813.9	1364.3	2592.5
AM745146.1	290803	4114.3	6562.8	5667.8	930.1	1948.6	2250.7
FJ712454.1	517813	226.1	291.0	1050.0	154.9	110.3	160.0
DQ831544.1	169282	3257.9	4748.6	3653.3	3161.3	5778.3	3877.0
EU981262.1	342198	2828.4	4149.1	6677.8	2385.8	1788.2	1647.6
AF354148.1	71200	530.4	1277.2	2641.8	542.3	1702.1	1696.4
EU981255.1	355558	2868.6	4217.2	9358.7	2939.2	8900.6	7867.3
AB294977.1	226332	1349.9	1632.0	3103.8	2092.4	900.8	1036.6

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GU118230.1 gg_id:540643 Threatened Corals Provide Microbial Habitats clone Dstr_P12
GQ246285.1 gg_id:590606 Temporal and spatial China North Yel Sea sediments clone Sd1-4
EU869410.1 gg_id:328130 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARI
EU287257.1 gg_id:257411 Pacific arctic surface sediment clone S11-74
AM745158.1 gg_id:296704 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
DQ831543.1 gg_id:168864 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
EU734932.1 gg_id:311410 assemblages sediment station DBSE Northern Bering Sea clone 023A38
EU981265.1 gg_id:346330 sulfate reducing living bench scale aquifer column water clone D18_SW
AY771968.1 gg_id:111554 marine surface sediment clone SD27
AY355305.2 gg_id:101832 epibiontic clone C6-B1
AM404380.1 gg_id:567796 Hydrocarbon-fueled sulfate reduction can sustain long-lived tubeworm aggregation
AY586398.1 gg_id:108445 fatty acid-degrading consortium clone FA-PB11
AY216446.1 gg_id:82114 temperate estuarine mud clone KM15
AY193139.1 gg_id:80324 marine sediment clone Bol88
EU528183.1 gg_id:281431 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
DQ677861.1 gg_id:243494 Blood Falls Subglacial Outf Taylor Glacier Antarctica subglacial outf clone BF99_C161
AB240495.1 gg_id:141610 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
AF050536.1 gg_id:10793 contaminated aquifer clone WCHB1-67
AY998140.1 gg_id:126281 Continental deep subsurface geochemically structured within alternating shale-sand
EU328056.1 gg_id:278259 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
EU652618.1 gg_id:279049 Seasonal variation microbial Yel Sea sediment clone C8S-16
GU302481.1 gg_id:569243 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
DQ521817.1 gg_id:161410 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexico
EU662614.1 gg_id:550521 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
EU290696.1 gg_id:241222 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
NR_026354.1 gg_id:571713 Desulfofustis glycolicus str. PerGlyS
EF632754.1 gg_id:249075 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
EU542499.1 gg_id:260510 Effects chemical structure concentration on pathways microbial during dechlorinatio
FJ264778.1 gg_id:341813 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AB100012.1 gg_id:99697 inactive deep-sea hydrothermal vent chimneys clone IndB4-24
AJ866934.1 gg_id:130219 Desulfobulbus mediterraneus str. NA62
AB252437.1 gg_id:156393 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I'
L42613.1 gg_id:10809 Desulforhopalus vacuolatus str. ltk10
FJ712433.1 gg_id:516762 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AY771961.1 gg_id:112020 marine surface sediment clone SP22
DQ831556.1 gg_id:164944 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
EU617846.1 gg_id:329676 Seasonal variation microbial Yel Sea sediment clone D13S-79
AY050586.1 gg_id:19356 MCB-contaminated groundwater-treating reactor clone GOUTA17
AJ241011.1 gg_id:10837 Norway:(Svalbard)Hornsund clone Sva0631
AM404330.1 gg_id:221162 aerobic and anaerobic methane oxidizers Arctic mud volcano(Haakon Mosby Mud V
FJ712434.1 gg_id:517763 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K

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GQ246285.1	590606	295.0	772.9	1882.4	489.3	188.6	330.8
EU869410.1	328130	5416.0	5593.5	5013.5	1978.9	2805.2	2653.2
EU287257.1	257411	4580.6	4484.7	2806.6	6323.6	7260.6	6665.7
AM745158.1	296704	4923.6	5552.9	7438.9	6967.6	11216.5	11523.1
DQ831543.1	168864	2237.8	1709.1	2461.5	1790.7	1390.9	952.5
EU734932.1	311410	3955.2	3248.4	6185.9	4407.3	6755.8	3335.3
EU981265.1	346330	11009.6	10110.0	9195.4	5343.9	7635.9	7961.4
AY771968.1	111554	2651.2	2428.1	3117.9	3295.4	679.6	887.6
AY355305.2	101832	1698.8	1783.3	3797.9	2139.3	2890.4	3803.0
AM404380.1	567796	3076.4	3463.2	6127.6	3317.0	5342.2	4595.9
AY586398.1	108445	924.6	742.4	2132.6	1735.8	136.3	257.9
AY216446.1	82114	782.7	478.0	2954.8	471.5	2261.5	910.3
AY193139.1	80324	2441.8	2129.6	1633.6	2849.6	5182.9	4943.2
EU528183.1	281431	3005.7	3669.6	3938.9	4149.7	2455.7	4756.7
DQ677861.1	243494	4446.2	6344.7	9262.0	3606.8	1230.2	2644.0
AB240495.1	141610	646.9	472.7	2007.3	351.7	1157.7	432.7
AF050536.1	10793	349.6	343.8	1077.1	246.6	309.4	455.7
AY998140.1	126281	772.3	959.7	955.3	1340.2	1575.8	911.6
EU328056.1	278259	4272.1	4511.3	6769.9	2777.3	2586.8	2377.8
EU652618.1	279049	5252.6	5925.7	4826.1	4850.7	3591.8	3329.0
GU302481.1	569243	129.9	355.2	2311.0	258.1	225.4	499.3
DQ521817.1	161410	23.2	26.9	42.3	45.8	57.2	14.6
EU662614.1	550521	651.9	2048.6	5934.4	1536.7	953.7	1548.8
EU290696.1	241222	3473.2	3703.9	4339.7	3039.1	6071.9	5093.9
NR_026354.1	571713	2614.3	2621.2	2875.4	4256.3	2481.1	3641.8
EF632754.1	249075	1125.7	1718.8	4439.3	1710.2	3245.3	2595.2
EU542499.1	260510	5754.1	6042.2	6611.8	5595.8	5562.2	3809.0
FJ264778.1	341813	12167.4	12800.1	6984.2	7298.9	8592.8	8117.8
AB100012.1	99697	440.7	687.5	3041.4	1135.3	325.9	458.2
AJ866934.1	130219	1763.2	2946.7	6062.9	1944.3	5085.8	4276.0
AB252437.1	156393	97.7	244.1	554.6	295.1	548.3	334.0
L42613.1	10809	38.3	72.7	256.6	56.7	57.4	33.3
FJ712433.1	516762	1150.1	1603.6	3332.2	971.7	1953.8	2113.2
AY771961.1	112020	6493.3	4507.8	3723.4	4954.6	6981.1	6220.2
DQ831556.1	164944	48.9	56.1	470.3	53.6	69.0	52.3
EU617846.1	329676	12236.7	10484.8	9334.6	7990.3	13116.3	10331.3
AY050586.1	19356	77.8	107.3	1376.6	117.3	114.1	147.3
AJ241011.1	10837	36.1	94.3	333.4	122.3	76.6	61.8
AM404330.1	221162	117.4	266.5	942.9	799.6	88.4	181.5
FJ712434.1	517763	83.2	260.0	553.9	121.6	272.7	459.0

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DQ811812.1 gg_id:161956 mangrove soil clone MSB-4F11
EU245867.1 gg_id:252562 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M7-D0
AM176869.1 gg_id:161369 Recovery mangrove sediment clone SZB64
EU287217.1 gg_id:252970 Pacific arctic surface sediment clone S11-34
FJ712587.1 gg_id:519783 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AY771966.1 gg_id:112333 marine surface sediment clone SQ20
FJ873362.1 gg_id:513064 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo
AF420365.1 gg_id:73580 hydrothermal sediment clone AF420365
EF422413.1 gg_id:203745 Desulfurivibrio alkaliphilus str. AHT2
DQ833475.1 gg_id:162310 detected analyses depth sediment Guanting Reservoir clone 5-48
AY771928.1 gg_id:135376 vertical d and intertidal mud flat Wadden Sea marine surface sediment clone LacK1
AY771960.1 gg_id:112173 marine surface sediment clone SN27
AB250577.1 gg_id:161256 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #5-8
AY327886.1 gg_id:90296 surface vent snail foot clone SF_C6-D1
AJ241013.1 gg_id:10827 Norway:(Svalbard)Hornsund clone Sva0999
AM950241.1 gg_id:567396 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec
DQ154829.1 gg_id:138936 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl
AB294967.1 gg_id:223812 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
EF687172.1 gg_id:282050 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir
FJ416079.1 gg_id:359718 sediments sediment station DBS1 Northern Bering Sea clone 162I41
AJ620509.1 gg_id:108099 Olavius crassitunicatus endosymbiont
AF420335.1 gg_id:71031 hydrothermal sediment clone AF420335
FJ264573.1 gg_id:335868 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
EU981263.1 gg_id:335188 sulfate reducing living bench scale aquifer column water clone D5_SW
AY771952.1 gg_id:112016 marine surface sediment clone SK1
GQ249525.1 gg_id:581436 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor
EU869406.1 gg_id:307864 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARI
AB426225.1 gg_id:259454 -situ identification study benzene-degrading s under methanogenic condition anaerc
AB100004.1 gg_id:79377 inactive deep-sea hydrothermal vent chimneys clone IndB2-42
FN396953.1 gg_id:561836 integrative isotopic approach study degradation mixed Mixed (US3-M) enriched grou
EU869423.1 gg_id:309672 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARI
EU283455.1 gg_id:279354 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A817
AB179691.1 gg_id:102062 groundwater 0.2 m-captured fraction clone KNA6-EB15
GU061178.1 gg_id:592956 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se
EU244009.1 gg_id:367854 16SrRNA probes river Leine sediment clone sl1127
AY771929.1 gg_id:111926 marine surface sediment clone LacK4
GQ246288.1 gg_id:512929 Temporal and spatial China North Yel Sea sediments clone Sd1-7
AM493255.1 gg_id:308423 Multiple symbionts two species co-occurring gutless oligochaete worms Mediterrar
AJ007373.1 gg_id:10840 environmental clone directly
DQ513028.1 gg_id:161392 Microbial life fluids ridge flank crustal fluid clone FS142-27B-02
GQ337170.1 gg_id:582065 Hydrography shapes biogeography deep Arctic Ocean water depth 410m clone CB1

DQ811812.1	161956	31.0	80.3	82.6	61.7	50.8	93.6
EU245867.1	252562	254.9	698.2	2053.9	187.8	137.7	220.6
AM176869.1	161369	124.4	240.2	2382.7	200.7	167.9	287.0
EU287217.1	252970	1015.9	1070.6	2090.9	673.7	877.9	1491.7
FJ712587.1	519783	1858.6	2080.1	2843.2	1586.8	736.9	2192.9
AY771966.1	112333	32.7	112.3	1567.8	84.4	84.2	38.2
FJ873362.1	513064	5040.8	5273.0	3509.3	3263.1	3245.8	4236.0
AF420365.1	73580	4400.3	4835.2	1204.4	4349.8	2406.9	2705.0
EF422413.1	203745	19.1	23.5	16.5	44.1	45.6	12.8
DQ833475.1	162310	500.6	823.3	4815.2	849.4	288.8	426.0
AY771928.1	135376	38.4	89.6	440.6	81.5	248.3	259.0
AY771960.1	112173	14699.3	15679.2	16379.4	12187.1	18007.4	14362.3
AB250577.1	161256	74.0	91.2	537.8	171.2	55.0	39.9
AY327886.1	90296	963.8	779.8	902.9	1972.1	652.1	1270.8
AJ241013.1	10827	7988.6	6711.3	5423.9	4736.7	6297.3	4972.0
AM950241.1	567396	40.9	187.3	2522.9	102.1	56.9	20.6
DQ154829.1	138936	643.8	1337.5	4416.4	964.3	4857.4	4792.3
AB294967.1	223812	1889.7	2196.7	2076.9	1410.6	1855.5	1484.0
EF687172.1	282050	371.9	579.3	3829.8	283.6	194.7	513.0
FJ416079.1	359718	6334.1	4225.2	2643.6	5695.7	8544.1	6269.9
AJ620509.1	108099	12.2	22.3	139.2	34.1	56.4	17.9
AF420335.1	71031	3961.9	6740.8	10180.0	4236.7	7980.0	7038.4
FJ264573.1	335868	825.9	945.1	3259.9	1104.2	1048.2	838.9
EU981263.1	335188	7699.2	8685.4	9565.6	5209.4	11193.3	9377.2
AY771952.1	112016	5652.4	6119.2	4556.1	5314.2	3549.3	4149.9
GQ249525.1	581436	4962.7	5461.6	4885.9	5828.1	7102.5	5100.2
EU869406.1	307864	5610.9	5622.1	5334.1	4763.2	4562.5	5406.4
AB426225.1	259454	2462.0	1934.6	4412.6	1992.8	2112.0	1416.9
AB100004.1	79377	2776.5	3452.7	4574.2	4355.9	4220.2	5010.2
FN396953.1	561836	65.1	364.5	5970.4	265.9	73.3	40.9
EU869423.1	309672	5921.3	6817.3	6123.8	4883.2	7321.4	5634.8
EU283455.1	279354	23.5	45.2	77.6	63.4	53.7	35.1
AB179691.1	102062	27.8	50.6	114.3	72.7	67.8	43.6
GU061178.1	592956	4381.4	5366.1	5521.4	3423.1	6847.6	6032.9
EU244009.1	367854	7539.0	9278.7	5445.0	8851.4	9638.7	9573.3
AY771929.1	111926	351.0	602.3	3117.2	588.1	184.1	264.7
GQ246288.1	512929	3019.3	4328.0	5648.3	3029.5	3186.5	3687.9
AM493255.1	308423	2280.2	2860.7	1223.2	3039.0	4638.1	6058.5
AJ007373.1	10840	1852.1	2642.2	3649.4	1471.9	3901.5	4145.3
DQ513028.1	161392	4861.5	5167.8	2525.8	1672.8	1011.5	1533.6
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AM997673.1 gg_id:548381 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
DQ009478.1 gg_id:125448 bacterioplankton clone SPOTSMAY03_890m2
L35504.1 gg_id:1673 Nitrospina gracilis str. Nb-211 Atlantic Ocean isolate
AY375081.1 gg_id:98326 deep sea sediment clone B108
EU236362.1 gg_id:299227 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91D6
DQ009430.1 gg_id:122261 bacterioplankton clone SPOTSFEB02_70m30
FJ615158.1 gg_id:588176 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 100m anoxi
EU491186.1 gg_id:260159 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
FJ205260.1 gg_id:513991 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
DQ396297.1 gg_id:154118 deep-sea octacoral clone ctg_NISA239
EU050846.1 gg_id:244986 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_02_21
GQ348628.1 gg_id:583192 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348702.1 gg_id:554642 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU617741.1 gg_id:339589 Seasonal variation microbial Yel Sea sediment clone C13S-128
GQ349342.1 gg_id:564925 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ009461.1 gg_id:116945 bacterioplankton clone SPOTSMAY03_500m10
DQ070818.1 gg_id:149964 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
DQ513042.1 gg_id:161152 Microbial life fluids ridge flank crustal fluid clone FS142-6B-02
AB015560.1 gg_id:1675 deep-sea sediment clone BD4-10
GU220750.1 gg_id:540822 Microbial mineralization and involved microbial Basin field temperature hydrotherm
GQ349282.1 gg_id:593656 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ154855.1 gg_id:139228 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl
FJ264670.1 gg_id:340510 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
EU937982.1 gg_id:317469 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY211659.1 gg_id:95547 Gulf Mexico seafloor sediment clone GoM GC185 508E
EU386020.1 gg_id:274277 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
DQ330990.1 gg_id:159337 Guerrero Negro hypersaline microbial mat clone 072DZ69
FJ484693.1 gg_id:512592 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
FJ264596.1 gg_id:303539 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
FN396681.1 gg_id:539102 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V
FJ902380.1 gg_id:594172 phreatic limestone sinkholes northeastern Mexico green biomat 8m deep cenote Car
EU385688.1 gg_id:268129 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
FJ716318.1 gg_id:551732 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept
FJ517130.1 gg_id:512958 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
DQ676358.1 gg_id:224366 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AY771962.1 gg_id:111849 marine surface sediment clone SR24
AJ306774.1 gg_id:66925 DCP-dechlorinating consortium clone SHA-72
GQ487920.1 gg_id:554266 Microbial metal soil polluted heavy metals clone T1-75
AB188771.1 gg_id:114153 cold seep sediment clone SB1-2
EU491434.1 gg_id:259879 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EF125402.1 gg_id:191519 soil naked tidal flat sediment near mangrove clone MSB-1E1

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AY375081.1	98326	5861.8	7748.7	5974.5	4061.5	4343.4	4340.3
EU236362.1	299227	4100.9	2667.1	1502.0	470.0	127.2	334.8
DQ009430.1	122261	161.9	398.5	665.2	147.5	130.4	303.4
FJ615158.1	588176	8733.2	12126.3	5776.2	7859.0	9518.2	9530.0
EU491186.1	260159	6901.3	6049.4	5628.8	3421.0	2091.5	2756.7
FJ205260.1	513991	8147.7	6032.1	8220.2	4726.9	2776.2	4751.0
DQ396297.1	154118	1299.8	1183.7	457.2	285.6	150.6	412.5
EU050846.1	244986	2576.1	3818.4	3746.0	1584.5	562.4	2909.0
GQ348628.1	583192	49.8	84.1	108.5	118.2	77.1	76.8
GQ348702.1	554642	4385.1	5775.6	3298.9	4073.4	3559.3	4574.5
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GQ349342.1	564925	27.6	58.0	100.9	59.9	72.3	54.1
DQ009461.1	116945	12010.4	10723.9	8879.3	7391.9	9417.5	8900.2
DQ070818.1	149964	4479.9	6471.8	4596.0	2520.1	1788.9	2642.1
DQ513042.1	161152	3918.8	3932.4	7482.6	3508.0	2336.9	4086.2
AB015560.1	1675	9370.6	7207.1	6049.3	3931.2	1794.2	2720.8
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GQ349282.1	593656	434.7	596.6	1583.0	337.4	200.0	803.3
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AY211659.1	95547	32.5	83.3	59.0	70.3	66.4	32.9
EU386020.1	274277	11101.3	12455.8	9386.2	9695.4	10493.9	11238.9
DQ330990.1	159337	1983.1	3349.3	3676.5	449.9	3615.7	5582.8
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FJ902380.1	594172	4907.7	4933.7	5075.2	6779.2	8341.9	7927.2
EU385688.1	268129	6599.3	8605.1	10554.3	7995.1	10742.7	7953.9
FJ716318.1	551732	4969.6	5173.5	4793.2	5580.7	3099.2	3321.0
FJ517130.1	512958	5590.9	5957.9	6594.6	3901.5	4620.6	4710.6
DQ676358.1	224366	2531.1	2976.8	3340.7	2595.9	2210.7	1841.7
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GQ487920.1	554266	10653.5	9053.7	7037.2	6669.9	5592.1	4608.1
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AB177175.1 gg_id:131091 seafloor methane hydrate clone ODP1230B22.09
AJ535229.1 gg_id:78077 marine sediment above hydrate ridge clone Hyd89-13 proteobacterium
EU617740.1 gg_id:338777 Seasonal variation microbial Yel Sea sediment clone C13S-10
DQ395025.1 gg_id:154412 harbor sediment clone VHS-B5-56
AB530224.1 gg_id:563571 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B
FJ793183.1 gg_id:532122 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB71
FJ484701.1 gg_id:562989 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AB291810.2 gg_id:244173 anaerobic benzene degrading enrichment which was d lotus field soil clone Hasda
FJ437911.1 gg_id:571145 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clor
FJ902095.1 gg_id:583726 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
AM176854.1 gg_id:159782 Recovery mangrove sediment clone SZB3
AY177804.1 gg_id:78912 Antarctic sediment clone LH5_30
AF543506.1 gg_id:58310 acid mine drainage clone BA9
DQ328619.1 gg_id:150232 microorganisms populating site extreme acid mine drainage sediment clone H11
EF409870.1 gg_id:205334 acid mine drainage clone YSK4-06
EU245455.1 gg_id:241617 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-G0
AF543496.1 gg_id:56683 acid mine drainage clone AS6
FN429806.1 gg_id:584068 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
EU385907.1 gg_id:274944 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
GQ246287.1 gg_id:583062 Temporal and spatial China North Yel Sea sediments clone Sd1-6
AB300126.1 gg_id:222448 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K
AJ301566.1 gg_id:28255 Germany:Schlema/Alberoda clone GR-296.I.86
EU491225.1 gg_id:273634 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
FJ746160.1 gg_id:572036 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
FJ205257.1 gg_id:512306 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
EU385892.1 gg_id:269081 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU925843.1 gg_id:327363 sediments sediment station DBS1 northern Bering Sea clone 034E59
FJ905645.1 gg_id:573989 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
AY093467.1 gg_id:63116 deep marine sediment clone MB-A2-137
FJ497387.1 gg_id:574286 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
DQ351799.1 gg_id:146139 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
AY592588.1 gg_id:105731 deep-sea mud volcano clone Napoli-1B-33; BC07-1B-33
EU491271.1 gg_id:261039 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ404601.1 gg_id:156317 contaminated sediment clone 656045
FJ746091.1 gg_id:570989 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EU937853.1 gg_id:352286 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
FJ746300.1 gg_id:508914 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EU048685.1 gg_id:250097 and archaeal surface marine sediment Slope South China Sea clone MD2896-B28
AY592672.1 gg_id:105663 deep-sea mud volcano clone Napoli-2B-50; BC07-2B-50
EU287051.1 gg_id:253719 Pacific arctic surface sediment clone B78-87
EU181482.1 gg_id:246264 Prokaryotic enhanced organic matter remineralization continental margin marine se

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AJ535229.1	78077	43.8	106.8	74.6	105.6	80.4	32.7
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DQ395025.1	154412	15244.9	15338.3	15933.3	12949.3	15494.6	14658.7
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FJ793183.1	532122	3094.2	4861.5	4239.0	3673.8	6296.4	1677.8
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AB291810.2	244173	638.6	551.2	785.7	977.0	1228.9	1080.2
FJ437911.1	571145	8893.6	8272.0	10034.1	7597.8	5054.0	6506.1
FJ902095.1	583726	12786.6	13617.1	11366.2	11754.2	17494.1	18188.2
AM176854.1	159782	863.3	1784.6	3891.1	892.9	767.0	2356.4
AY177804.1	78912	1583.1	2171.0	4085.0	2557.5	1214.1	1983.7
AF543506.1	58310	4273.3	6172.2	8921.5	5428.3	6003.3	4645.3
DQ328619.1	150232	4269.9	4721.2	3304.2	5589.6	7650.6	6514.4
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EU245455.1	241617	530.1	500.5	193.4	187.7	70.3	101.5
AF543496.1	56683	7651.2	12127.3	6029.2	6433.2	10360.5	9735.6
FN429806.1	584068	337.6	1252.2	3937.4	297.9	269.8	1230.0
EU385907.1	274944	9695.7	10511.7	3785.7	6243.9	6353.8	4931.1
GQ246287.1	583062	17.1	22.3	19.2	40.1	48.4	21.6
AB300126.1	222448	72.4	102.1	54.8	69.3	71.9	44.2
AJ301566.1	28255	89.5	242.3	141.5	115.2	165.0	188.9
EU491225.1	273634	1373.2	1804.8	2612.4	1409.9	1039.9	2910.2
FJ746160.1	572036	3193.1	4712.8	6138.7	1880.9	4105.0	4539.8
FJ205257.1	512306	3564.8	4568.5	3732.7	2573.8	2712.2	2719.0
EU385892.1	269081	9682.4	9648.1	9241.8	6797.6	7503.1	6088.9
EU925843.1	327363	3143.9	4586.6	9640.4	3808.8	6041.2	6428.4
FJ905645.1	573989	1535.4	2608.5	3684.6	1154.7	2901.5	3512.3
AY093467.1	63116	1752.8	5746.4	4133.3	2033.7	1222.6	2166.1
FJ497387.1	574286	4354.5	5356.7	8925.3	2463.0	2122.9	2787.8
DQ351799.1	146139	181.7	195.5	408.8	742.2	160.8	453.4
AY592588.1	105731	490.2	690.7	942.2	872.1	165.0	474.4
EU491271.1	261039	1938.2	3212.1	3742.1	2124.0	3816.6	3101.5
DQ404601.1	156317	12001.8	13370.1	12294.4	6194.9	6716.0	7914.9
FJ746091.1	570989	8748.8	9954.6	8059.1	8134.2	10270.0	8463.9
EU937853.1	352286	2034.7	3355.3	5295.7	2391.8	2836.0	2013.6
FJ746300.1	508914	3623.6	4634.3	8204.6	2902.1	3312.6	4496.2
EU048685.1	250097	9838.0	11392.9	11517.1	8299.1	11127.3	12108.8
AY592672.1	105663	66.5	160.7	34.5	53.0	65.2	42.9
EU287051.1	253719	2960.3	3449.7	3189.3	2491.3	8399.4	6453.3
EU181482.1	246264	2912.5	4353.3	7810.0	3407.6	3202.3	3944.9

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s__Desulfovibrio alaskensis	57320

AY592130.1 gg_id:100278 marine ANAMMOX sediment clone AY592130
FJ755771.1 gg_id:586023 vertical archaeal water and Lake Taihu sediment clone LT-SB-B77
X99235.1 gg_id:10401 Desulfohalobium retbaense str. HR100 (DSM 5692T)
U48244.1 gg_id:10400 Desulfohalobium retbaense str. DSM 5692
EU296539.1 gg_id:241507 Desulfonatronospira aceticus str. AHT 6
X99234.1 gg_id:10404 Desulfonatronovibrio hydrogenovorans str. Z-7935 (DSM 9292T)
GU196828.1 gg_id:557238 Desulfonatronovibrio sp. str. AHT21
EF644847.1 gg_id:299192 genes and citrate lyase deep-sea microbial MAR Rainbow hydrothermal vent system
AF524933.1 gg_id:74638 Desulfonauticus submarinus str. 6N
FJ194951.1 gg_id:329685 Desulfonauticus sp. str. DSM 4206
EU245681.1 gg_id:241136 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M4-F1(
DQ103666.1 gg_id:136882 hypersaline endoevaporitic microbial mat clone E6bG07
EU245471.1 gg_id:253107 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-A0:
EU245401.1 gg_id:237109 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-C0:
AB264617.1 gg_id:167257 Desulfothermus okinawensis str. TFISO9 (= JCM 13304 = DSM 17375)
NR_025378.1 gg_id:537936 Desulfomicrobium orale str. DSM 12838
AY464939.1 gg_id:100488 Desulfocaldus terraneus str. P6.2
DQ069204.1 gg_id:130717 gold mine clone MAB25
AJ277886.1 gg_id:33526 Desulfomicrobium escambiense str. DSM 10707T
DQ069227.1 gg_id:128063 gold mine clone SRB5
Y14594.1 gg_id:10408 Desulfonatronum lacustre str. z-7951
AY725424.1 gg_id:103231 Desulfonatronum cooperatoris str. Z-9799
GQ863488.1 gg_id:550045 Desulfonatronum sp. str. HSRB-L1
DQ088749.1 gg_id:129416 subsurface clone BE325FW032701CTS_hole1-63
GQ493712.1 gg_id:546485 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ363013.1 gg_id:361170 feces adult twins and mothers; TS148 clone TS148_a01h07
AY978908.1 gg_id:121944 human transverse colon mucosal biopsy clone NG04
EF602909.1 gg_id:230078 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU454891.1 gg_id:305445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S
EU505347.1 gg_id:258794 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02h11
EU452762.1 gg_id:309442 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EF096212.1 gg_id:180715 mouse cecum clone obob1_aaa02f06
AY993240.1 gg_id:129830 mouse cecum clone C21_k13
EF097816.1 gg_id:184560 mouse cecum clone SWPT20_aaa04c06
AY991087.1 gg_id:131193 mouse cecum clone C13_O03
EU455583.1 gg_id:344389 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EF097361.1 gg_id:199580 mouse cecum clone SWPT19_aaa01e10
DQ071477.1 gg_id:234242 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc14
DQ308598.1 gg_id:148623 sheep rumen enrichment clone 196.G06
EU659693.1 gg_id:283392 Desulfovibrio africanus str. SR-1
DQ365927.1 gg_id:154031 Desulfovibrio alaskensis str. IMP-7760

AY592130.1	100278	8894.7	8681.4	7534.2	7336.4	10403.8	10018.8
FJ755771.1	586023	1514.4	2393.4	5094.8	3137.0	1019.1	1776.2
X99235.1	10401	134.6	160.6	214.9	237.5	217.3	183.6
U48244.1	10400	6841.9	7364.1	5006.5	5166.4	9564.8	8660.6
EU296539.1	241507	3840.5	5324.0	6109.2	2654.8	3773.7	3937.2
X99234.1	10404	281.7	547.2	491.6	259.1	431.9	141.4
GU196828.1	557238	5052.8	4730.4	8572.6	2738.4	2989.7	4922.0
EF644847.1	299192	5791.1	5450.7	8583.8	6062.2	6728.2	4962.8
AF524933.1	74638	35.1	36.9	53.9	54.1	73.3	38.3
FJ194951.1	329685	1714.9	3080.5	6881.8	2112.1	2458.6	2573.9
EU245681.1	241136	1310.3	2048.9	3483.2	879.0	965.3	1813.7
DQ103666.1	136882	3289.9	3220.5	2851.9	1925.1	2855.7	2922.8
EU245471.1	253107	7246.9	8984.5	9051.9	6708.3	5584.4	6787.5
EU245401.1	237109	2929.4	3252.4	5235.5	1928.3	1354.7	2256.0
AB264617.1	167257	36.8	40.4	45.1	68.2	125.3	59.6
NR_025378.1	537936	2769.3	2613.6	686.8	731.0	1354.4	1438.8
AY464939.1	100488	10810.7	10249.7	11072.8	8573.3	9537.8	8449.4
DQ069204.1	130717	18607.9	20000.6	18930.7	17183.5	18131.0	14663.6
AJ277886.1	33526	1039.3	1406.6	2241.1	881.1	2356.1	2078.6
DQ069227.1	128063	1058.1	1443.2	1596.0	676.1	2422.0	1551.1
Y14594.1	10408	36.5	46.2	50.8	58.2	66.8	28.0
AY725424.1	103231	1111.4	1819.5	1408.3	1625.2	1019.2	1355.4
GQ863488.1	550045	4012.7	4305.9	4823.9	4437.7	4288.3	5212.5
DQ088749.1	129416	1425.0	1724.1	3007.6	2345.5	776.4	859.8
GQ493712.1	546485	3752.6	2864.1	4636.7	5176.7	5112.3	3532.9
FJ363013.1	361170	1695.4	2140.8	2732.6	1794.8	4297.9	2192.4
AY978908.1	121944	1299.5	535.3	1957.0	1593.1	1475.1	984.8
EF602909.1	230078	80.6	134.8	175.7	72.4	81.4	73.9
EU454891.1	305445	6846.5	7124.5	6261.5	7958.6	7775.2	7247.4
EU505347.1	258794	5427.6	5844.7	1887.7	5636.6	5951.6	4349.5
EU452762.1	309442	13340.9	13778.1	9320.6	12081.4	13629.2	12124.4
EF096212.1	180715	12375.1	14010.0	9241.0	10569.7	13502.9	11460.4
AY993240.1	129830	3277.1	3667.9	3654.1	4033.6	3024.1	3083.9
EF097816.1	184560	2503.5	3330.1	4558.4	1618.7	2888.2	4239.1
AY991087.1	131193	3178.6	3229.9	2413.3	3704.2	3789.3	4826.6
EU455583.1	344389	8063.8	7802.6	8702.6	9704.0	7223.5	8550.7
EF097361.1	199580	3410.4	2388.5	2183.9	3293.5	6746.7	5140.0
DQ071477.1	234242	22.4	33.5	29.0	36.7	55.4	26.7
DQ308598.1	148623	34.7	104.3	128.4	107.5	125.6	118.8
EU659693.1	283392	241.7	359.7	422.0	628.8	1424.9	2051.3
DQ365927.1	154031	2854.6	2387.4	3647.3	1331.7	1674.1	2199.4

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s__Desulfovibrio bastinii	56460
s__Desulfovibrio bastinii	56657
s__Desulfovibrio capillatus	57274
s__Desulfovibrio cavernae	56859
s__Desulfovibrio dechloracetivorans	57137
s__Desulfovibrio dechloracetivorans	57405
s__Desulfovibrio dechloracetivorans	57771
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s__Desulfovibrio desulfuricans	56853
s__Desulfovibrio desulfuricans	57107
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s__Desulfovibrio halophilus	56766
s__Desulfovibrio indonesiensis	56965
s__Desulfovibrio magneticus	56592
s__Desulfovibrio mexicanus	57614
s__Desulfovibrio putealis	56948
s__Desulfovibrio putealis	57091
s__Desulfovibrio putealis	57341
s__Desulfovibrio putealis	57455
s__Desulfovibrio salexigens	56541
s__Desulfovibrio senezii	56493
s__Desulfovibrio sulfodismutans	57162
s__Desulfovibrio vulgaris	57465
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s__unclassified	56537

AF423185.1 gg_id:34507 Toluene-degrading methanogenic consortium clone Eub 5 consortium
EU251185.1 gg_id:248227 Desulfovibrio sp. str. ds2-2
U53462.1 gg_id:10445 Desulfovibrio bastinii str. SEBR 4225
NR_025766.1 gg_id:533801 Desulfovibrio bastinii str. SRL4225; DSM 16055
FJ024714.1 gg_id:330860 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp
DQ109922.1 gg_id:142678 Sulfate-reducing mats: Changing paradigms new discoveries salt pond nonlithifying
AY281345.1 gg_id:87605 Desulfovibrio sp. str. ANP3
U85475.1 gg_id:10430 Desulfovibrio sp. str. BG50
AF230530.1 gg_id:30839 Desulfovibrio dechloracetivorans
FJ823871.1 gg_id:516368 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
GQ503772.1 gg_id:577487 uranium mine tailing pond inlet water clone Jdgsrb019
GQ503807.1 gg_id:585949 effulent treatment plant inlet clone Jdgsrb054
AF098671.1 gg_id:10516 Desulfovibrio desulfuricans
AJ295680.1 gg_id:74474 Desulfovibrio intestinalis str. JG-G12
DQ526427.1 gg_id:160710 Desulfovibrio desulfuricans str. EFX-DES
GQ503792.1 gg_id:591259 uranium mine tailing pond inlet water clone Jdgsrb039
GQ503771.1 gg_id:577327 uranium mine tailing pond inlet water clone Jdgsrb018
GQ898871.1 gg_id:572458 strain Desulfovibrio enrichment medium DSMZ 163 inoculated water Jaduguda Urar
GQ503812.1 gg_id:539624 effulent treatment plant inlet clone Jdgsrb059
GQ503798.1 gg_id:564326 uranium mine tailing pond inlet water clone Jdgsrb045
FJ823874.1 gg_id:530538 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
FJ823870.1 gg_id:521886 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
AJ544687.2 gg_id:80009 Desulfovibrio brasiliensis str. LVform1
NR_025977.1 gg_id:570680 Desulfovibrio gabonensis str. SEBR 2840; DSM 10636
AP010904.1 gg_id:384156 Desulfovibrio magneticus str. RS-1
AJ582758.1 gg_id:96567 Desulfovibrio ferrireducens str. CY2
GU139267.1 gg_id:542453 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth
GQ402775.1 gg_id:567650 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF562565.1 gg_id:235762 stable microbial consortia capable degrading complex organic matter paper pulp colu
NR_029118.1 gg_id:592620 Desulfovibrio putealis str. B7-43; DSM 16056
CP001649.1 gg_id:516164 Desulfovibrio salexigens str. DSM 2638
AF050100.1 gg_id:10448 Desulfovibrio senezii str. CVL; DSM 8436
AY340820.1 gg_id:91518 sulfate-reducing fluidized-bed reactor clone SR_FBR_E5
X86689.1 gg_id:10505 Desulfovibrio sp str. DMB
GQ898881.1 gg_id:585282 strain Desulfovibrio enrichment medium DSMZ 163 inoculated water East Calcutta v
AB062810.1 gg_id:23507 termite gut homogenate clone BCf11-19
GQ502605.1 gg_id:582695 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf6-
X95230.2 gg_id:10429 Desulfovibrio aespoeensis str. Aspo2
Y18049.1 gg_id:10442 Desulfovibrio zosterae
EU885150.1 gg_id:327333 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB2
FM178807.1 gg_id:351705 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu

AF423185.1	34507	4132.4	6496.8	3396.4	2771.6	5348.6	3939.2
EU251185.1	248227	35.7	59.7	166.6	70.6	105.6	68.0
U53462.1	10445	727.7	924.8	1297.9	1104.2	408.8	357.5
NR_025766.1	533801	1371.4	1451.0	445.8	375.8	1870.4	1197.9
FJ024714.1	330860	10372.2	9611.3	5685.9	8554.8	9918.4	9450.1
DQ109922.1	142678	198.1	86.1	326.4	106.9	302.8	198.4
AY281345.1	87605	1636.7	2200.8	3351.5	1681.8	1910.3	2095.4
U85475.1	10430	118.1	318.8	2353.0	227.4	239.2	223.8
AF230530.1	30839	11384.7	12091.9	8912.6	9166.7	11082.7	10360.1
FJ823871.1	516368	5105.5	4998.7	4150.7	6517.6	9987.9	9809.3
GQ503772.1	577487	1581.7	1702.3	2478.3	1298.2	1163.5	1421.8
GQ503807.1	585949	40.1	62.4	150.2	67.3	81.5	42.9
AF098671.1	10516	943.4	2041.4	5279.1	1338.9	563.9	1200.9
AJ295680.1	74474	4516.0	4303.8	6412.0	4613.0	3876.2	2840.2
DQ526427.1	160710	124.1	470.8	1297.2	194.5	723.8	512.0
GQ503792.1	591259	4842.1	5675.4	355.7	7080.6	8077.1	6140.8
GQ503771.1	577327	8398.6	10162.0	3973.4	7096.5	4316.7	4720.8
GQ898871.1	572458	3759.7	4593.4	3441.9	3091.3	4124.3	3586.4
GQ503812.1	539624	5523.6	7339.7	2298.9	3721.3	3328.6	2763.8
GQ503798.1	564326	11191.0	13233.2	11167.1	9168.3	10314.2	7883.1
FJ823874.1	530538	12048.7	11501.5	7423.5	10673.9	11444.6	8643.1
FJ823870.1	521886	2015.3	2894.8	969.6	834.1	3894.0	2088.6
AJ544687.2	80009	498.6	504.6	809.4	527.3	1018.4	286.3
NR_025977.1	570680	53.7	105.6	321.5	90.9	82.2	49.1
AP010904.1	384156	2986.1	4505.7	6741.8	4244.1	2787.4	5000.8
AJ582758.1	96567	240.6	993.6	4873.2	423.6	204.6	995.1
GU139267.1	542453	10126.1	8628.1	8365.3	11925.1	13033.3	14220.9
GQ402775.1	567650	2066.5	3048.9	5276.5	1081.8	2166.5	1912.4
EF562565.1	235762	7746.4	8346.1	11453.2	7577.3	8806.1	7693.0
NR_029118.1	592620	67.4	258.5	1501.0	98.2	201.1	230.7
CP001649.1	516164	3086.2	3241.8	1627.2	2178.7	2532.0	2323.8
AF050100.1	10448	19.3	37.8	66.3	50.1	58.1	19.2
AY340820.1	91518	59.4	148.4	264.4	87.7	101.1	44.3
X86689.1	10505	3148.4	4088.5	2765.4	4286.2	3232.5	3904.8
GQ898881.1	585282	1405.8	2626.6	1641.1	1606.3	1748.4	2441.0
AB062810.1	23507	4753.8	5762.7	7659.9	11068.4	7024.8	5563.9
GQ502605.1	582695	3717.8	4534.3	3665.1	3110.8	4254.1	2881.2
X95230.2	10429	1304.1	1876.8	1774.2	985.3	3312.7	2193.4
Y18049.1	10442	107.6	184.0	372.3	308.5	145.2	293.5
EU885150.1	327333	5720.1	5184.2	3932.0	2840.8	3557.0	3655.8
FM178807.1	351705	388.3	908.7	2225.4	325.2	238.3	304.4

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EU885151.1 gg_id:331480 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB3
GU174149.1 gg_id:558603 Microbial Bactrian camel estimated rumen clone XJC38
EU885102.1 gg_id:304312 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3C12
EU885154.1 gg_id:337642 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AF9
FJ225426.1 gg_id:364203 Desulfovibrio sp. str. H1
EF577029.1 gg_id:264685 Desulfovibrio defluvii str. RB22
FJ440030.1 gg_id:510683 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou
AM418397.1 gg_id:179230 Desulfohimalaya abdulkalamii str. pwc
AY746987.1 gg_id:100353 Desulfovibrio oxyvorans str. DvO5
FJ172813.1 gg_id:354049 Qinghai Yak Ruminal and Fungi China rumen clone RB-4C1
EU850487.1 gg_id:319780 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF252
EU245278.1 gg_id:257276 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B11
EU885153.1 gg_id:316313 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB12
U90726.1 gg_id:10427 Desulfovibrio profundus str. DSM 11384 500-1
AF053752.1 gg_id:10462 Desulfovibrio burkinensis str. HDv; DSM 6830
EU775070.1 gg_id:308451 Francois Langur feces clone FL_2aaa02h01
AB234535.1 gg_id:147874 termite gut homogenate clone MgMjR-025
AB192287.1 gg_id:141741 termite gut homogenate clone RPK-26
AF056091.1 gg_id:10518 Desulfovibrio sp. str. UNSW3caefatS
NR_026303.1 gg_id:562366 Desulfovibrio vietnamensis str. G3 100 ID95-371
AB470954.1 gg_id:536904 Desulfovibrio sp. str. r49
EU885140.1 gg_id:350456 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2C5
EU885104.1 gg_id:348053 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3G4
AY649785.1 gg_id:102334 Desulfovibrio alkalitolerans str. RT2
CP000112.1 gg_id:143024 Desulfovibrio desulfuricans str. G20
FJ655908.1 gg_id:558435 Desulfovibrio sp. str. I9
FJ202471.1 gg_id:305033 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AF053751.1 gg_id:10470 Desulfovibrio alcoholovorans str. DSM 5433
AF192152.1 gg_id:51535 Desulfovibrio piger str. ATCC29098
U53464.1 gg_id:10452 Desulfovibrio gracilis str. SEBR 6116
EU616635.1 gg_id:321186 digestive-tract microbiota Hirudo orientalis european medicinal leech Desulfovibrio c
DQ447183.2 gg_id:156761 Desulfovibrio gigas str. DSM 1382; ATCC 19364
EU885143.1 gg_id:335081 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB10
AY726757.3 gg_id:107875 Desulfovibrio sp. SB1
DQ422859.1 gg_id:161406 Desulfovibrio bizertensis str. MB3
AF371871.1 gg_id:30569 swine intestine clone p-2918-6C5
EU885152.1 gg_id:341908 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AE3
EU885101.1 gg_id:322341 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3F9
AJ132721.1 gg_id:111852 deep-sea hydrothermal chimney clone CHA3-114
NR_025038.1 gg_id:564993 Desulfovibrio inopinatus str. HHQ 20; DSM 10711
AY274444.1 gg_id:104557 Desulfovibrio sp. str. HS2

EU885151.1	331480	3179.9	2923.7	2543.3	392.7	3958.0	4520.6
GU174149.1	558603	3157.9	3223.8	8847.5	2375.3	2514.7	2911.7
EU885102.1	304312	1290.8	1849.0	1813.8	870.8	1614.5	1517.7
EU885154.1	337642	6139.1	7163.4	6345.6	5320.5	5819.9	5116.5
FJ225426.1	364203	12354.3	12238.6	10242.6	9990.1	13818.2	12194.1
EF577029.1	264685	5269.3	5855.3	6482.0	4623.3	5258.2	5585.6
FJ440030.1	510683	328.4	876.6	1798.2	550.4	289.9	778.3
AM418397.1	179230	48.8	53.1	62.1	87.9	99.5	52.6
AY746987.1	100353	2313.6	3436.6	5315.0	3510.7	2054.8	3640.5
FJ172813.1	354049	9987.4	8864.6	5816.2	9186.4	11501.2	7970.6
EU850487.1	319780	2277.0	2601.0	8078.0	3290.4	3495.0	2944.7
EU245278.1	257276	108.6	235.2	404.6	185.3	216.6	244.5
EU885153.1	316313	9628.6	7733.1	5585.7	4209.5	2333.4	4379.5
U90726.1	10427	970.0	1462.7	2267.2	657.1	1914.2	1306.5
AF053752.1	10462	203.0	421.8	3555.3	375.7	527.2	332.1
EU775070.1	308451	56.2	177.4	289.1	88.2	142.5	169.2
AB234535.1	147874	6078.3	6193.0	4009.6	3741.9	2956.1	3558.8
AB192287.1	141741	48.9	171.8	289.0	70.6	91.0	102.0
AF056091.1	10518	84.3	227.5	229.6	124.9	179.6	570.2
NR_026303.1	562366	8993.8	7154.1	7965.7	6752.4	6124.6	8193.5
AB470954.1	536904	1949.4	2128.6	4324.0	1224.8	2166.8	2837.6
EU885140.1	350456	6751.3	7450.8	6007.3	5585.0	6150.8	3814.5
EU885104.1	348053	1374.4	1900.7	3348.2	2196.5	2332.8	2384.2
AY649785.1	102334	49.5	78.2	40.9	61.8	96.8	79.4
CP000112.1	143024	1032.7	839.6	2337.0	599.6	617.7	836.6
FJ655908.1	558435	76.7	107.5	101.0	102.2	107.6	57.3
FJ202471.1	305033	3867.7	4449.6	448.4	602.7	1043.3	770.1
AF053751.1	10470	3059.0	5642.5	7014.2	2797.8	3014.3	5887.8
AF192152.1	51535	192.3	480.7	765.9	93.5	88.8	262.9
U53464.1	10452	5054.9	5284.1	4461.1	3762.3	6005.3	4462.7
EU616635.1	321186	2542.7	2881.7	3126.0	1528.1	4290.9	2799.7
DQ447183.2	156761	121.7	281.3	432.7	134.3	135.3	157.8
EU885143.1	335081	6755.2	4656.1	7925.6	4543.3	5102.6	6140.0
AY726757.3	107875	1439.2	1019.4	1040.8	675.8	300.7	304.6
DQ422859.1	161406	27.8	32.3	25.4	44.7	60.6	28.1
AF371871.1	30569	30.6	41.9	30.2	60.5	79.1	40.8
EU885152.1	341908	3198.3	1862.5	4454.7	2110.1	3131.8	2295.3
EU885101.1	322341	2491.5	3001.2	6426.3	2462.0	4448.0	2686.4
AJ132721.1	111852	432.8	653.1	407.6	303.9	291.0	179.3
NR_025038.1	564993	54.1	160.4	357.2	116.9	131.5	146.5
AY274444.1	104557	1607.1	2127.6	3156.4	1476.3	1572.1	2045.6

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DQ186200.2 gg_id:243561 Desulfovibrio carbinoliphilus str. D41
Y11984.3 gg_id:28397 Desulfovibrio alaskensis str. NCIMB 13491
DQ841177.2 gg_id:195717 Desulfovibrio sp. str. AS36
EF453987.2 gg_id:225093 termite hindgut clone 290cost002-P3L-1410
AM947130.1 gg_id:270241 Desulfovibrio marrakechensis str. DSM 19337
CP001197.1 gg_id:529124 Desulfovibrio vulgaris 'Miyazaki F' str. Miyazaki F
EF123506.1 gg_id:257510 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
U85468.1 gg_id:10463 Desulfovibrio sp. str. BG6
AF228128.2 gg_id:43170 Desulfovibrio sp. str. Pr1.2
GQ502595.1 gg_id:585650 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf6-
NR_025765.1 gg_id:576099 Desulfovibrio longus str. SEBR 2582; DSM 6739
AY274449.1 gg_id:105315 Desulfovibrio ferrophilus str. IS5
X95231.1 gg_id:10444 Bacterial sp.
NC_008011.1 gg_id:159002 Lawsonia intracellularis str. PHE/MN1-00
AY976442.1 gg_id:118641 human ascending colon mucosal biopsy clone LZ39
GQ867364.1 gg_id:588730 and prevalence blaTEM genes Arctic seals colon content clone WSp127
EU381557.1 gg_id:265414 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
FJ833256.1 gg_id:572886 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_22F03
EU468458.1 gg_id:287520 okapi feces clone OK1_a06
EU461101.1 gg_id:303251 red kangaroo feces clone KO1_aai44b11
AB234532.1 gg_id:146574 termite gut homogenate clone MgMjD-084
AB089110.1 gg_id:78137 termite gut homogenate clone Rs-N35 proteobacterium
AB192288.1 gg_id:143786 termite gut homogenate clone RPK-66
X99501.1 gg_id:10486 Desulfovibrio sp. str. STL1
FJ374255.1 gg_id:365000 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
AB234538.1 gg_id:149936 termite gut homogenate clone MgMjR-064
AB089109.1 gg_id:78006 termite gut homogenate clone Rs-M89 proteobacterium
EF454896.2 gg_id:220622 termite hindgut clone 290cost002-P3L-618
X99504.1 gg_id:10485 Desulfovibrio sp. str. STL6
FJ374258.1 gg_id:361169 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
AB089105.1 gg_id:78148 termite gut homogenate clone Rs-K75
AY532164.1 gg_id:137367 Desulfovibrio sp. str. ZIRB-2
AB234531.1 gg_id:148238 termite gut homogenate clone MgMjD-065
Y16942.1 gg_id:10572 Desulfurella propionica str. U-8 (DSM 10410)
Y16941.1 gg_id:10573 Desulfurella kamchatkensis str. K-119 (DSM 10409)
NR_026109.1 gg_id:566496 Desulfurella acetivorans str. A63; DSM 5264
Y18292.1 gg_id:51780 Hippea maritima str. MH2T
FJ264595.1 gg_id:343915 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AB294284.1 gg_id:207880 Microbial structure deep coal seem groundwater clone YWB15
AY062880.1 gg_id:38853 environmental electrode surface clone d14
EU052251.1 gg_id:240954 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe

DQ186200.2	243561	2942.3	4259.6	6955.8	4448.3	3317.7	5233.4
Y11984.3	28397	2703.6	2074.5	2467.9	1157.2	2245.4	2435.8
DQ841177.2	195717	4250.7	4395.7	6437.4	4163.1	6544.4	7948.7
EF453987.2	225093	34.4	31.3	45.6	61.0	64.2	42.1
AM947130.1	270241	2228.0	3102.2	4843.7	3994.9	2826.7	4398.8
CP001197.1	529124	29.7	44.1	95.9	60.2	159.4	75.4
EF123506.1	257510	2270.3	3699.5	4936.2	2639.9	2929.3	2943.6
U85468.1	10463	1843.2	3558.7	4810.9	3431.4	6955.2	8519.3
AF228128.2	43170	30.8	59.8	167.9	81.3	71.6	48.2
GQ502595.1	585650	2749.2	3555.1	7140.8	2803.4	2190.4	2067.7
NR_025765.1	576099	4495.3	3261.6	4045.1	5096.6	7935.8	5193.7
AY274449.1	105315	462.5	554.0	2742.3	502.4	719.6	596.2
X95231.1	10444	2566.1	2019.7	618.7	980.5	795.0	380.8
NC_008011.1	159002	260.0	389.2	865.6	332.8	485.0	499.4
AY976442.1	118641	22.9	49.7	104.4	57.5	59.6	38.0
GQ867364.1	588730	2036.4	2759.4	8365.0	3856.8	4569.8	3586.1
EU381557.1	265414	3381.2	3499.4	2283.8	5319.9	3942.7	3535.0
FJ833256.1	572886	3614.6	4234.6	3413.1	3299.6	4021.8	3923.4
EU468458.1	287520	9121.0	10675.8	7064.6	5986.4	11976.2	10062.8
EU461101.1	303251	40.2	44.1	47.1	85.4	76.9	42.0
AB234532.1	146574	21.9	152.0	453.9	112.9	241.2	315.4
AB089110.1	78137	7598.0	8661.4	5046.2	3561.9	5804.9	4925.7
AB192288.1	143786	28.7	42.1	119.9	50.0	89.4	30.0
X99501.1	10486	66.9	90.5	93.7	97.2	113.0	94.4
FJ374255.1	365000	1218.6	1382.8	1093.1	425.1	569.5	588.1
AB234538.1	149936	33.5	44.3	60.3	59.0	66.0	27.2
AB089109.1	78006	861.8	1084.3	1223.7	837.7	780.9	885.7
EF454896.2	220622	495.5	679.6	925.2	1573.7	1005.0	1303.4
X99504.1	10485	46.6	39.5	86.4	70.7	93.2	142.7
FJ374258.1	361169	203.2	439.2	1500.2	249.9	585.4	1228.7
AB089105.1	78148	80.7	85.9	97.2	90.5	104.0	51.7
AY532164.1	137367	24.4	25.3	124.0	32.6	44.4	31.3
AB234531.1	148238	68.3	69.0	97.2	81.8	87.2	49.8
Y16942.1	10572	14923.2	15402.2	10676.1	10781.2	14760.2	11908.8
Y16941.1	10573	4915.5	7001.6	3117.9	2389.4	4735.6	3187.3
NR_026109.1	566496	13900.6	19153.6	11488.5	10009.2	18482.2	13619.9
Y18292.1	51780	33.5	100.8	233.4	61.7	71.2	51.2
FJ264595.1	343915	3039.0	4868.7	2813.5	2893.9	5287.7	2253.4
AB294284.1	207880	255.7	655.5	1417.7	360.3	1089.0	2339.0
AY062880.1	38853	1160.2	1875.4	2286.6	1019.7	1145.4	1630.4
EU052251.1	240954	8933.1	10924.8	9212.8	9232.0	8457.3	9516.3

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s__Geobacter bemidjiensis	56521
s__Geobacter lovleyi	56754
s__Geobacter metallireducens	56814
s__Geobacter psychrophilus	56468
s__Geobacter sp. FRC-32	56613
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s__Geobacter sp. FRC-32	57080

NR_026407.1 gg_id:575070 Desulfuromonas thiophila str. NZ27 DSMZ 8987
EU246142.1 gg_id:235638 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-B12
AY062875.1 gg_id:52449 environmental electrode surface clone d9
AJ519664.1 gg_id:76391 uranium mill tailings soil sample clone GuBH2-AG-114 proteobacterium
AB294287.1 gg_id:210461 Microbial structure deep coal seem groundwater clone YWB18
X79415.1 gg_id:10692 Desulfuromusa succinoxidans str. Gylac (DSM 8270)
GQ433952.1 gg_id:554572 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst
EU542456.1 gg_id:263005 Effects chemical structure concentration on pathways microbial during dechlorinatio
NR_026154.1 gg_id:552396 Pelobacter acidigallici str. MaGal12T; DSM 2377
GU180167.1 gg_id:581956 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
NR_026479.1 gg_id:539100 Malonomonas rubra str. GraMal1; DSM 5091
FJ638573.1 gg_id:538924 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
AY280424.1 gg_id:101417 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
EU386013.1 gg_id:262433 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
GQ246309.1 gg_id:511753 Temporal and spatial China North Yel Sea sediments clone Sd1-28
EU052244.1 gg_id:237074 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe
DQ677843.1 gg_id:245056 Blood Falls Subglacial Outf Taylor Glacier Antarctica subglacial outf clone BF99_C24
DQ309326.1 gg_id:145062 Desulfuromonas alkaliphilus str. Z-0531
AJ441215.1 gg_id:74843 hydrothermal vent polychaete mucous clone P. palm C/A 79
EU052243.1 gg_id:252121 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe
AY187308.1 gg_id:102591 Pelobacter masseliensis
EU617856.1 gg_id:346218 Seasonal variation microbial Yel Sea sediment clone C13S-139
AB355057.1 gg_id:236199 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma
AY998187.1 gg_id:115871 Continental deep subsurface geochemically structured within alternating shale-sand
AY515473.1 gg_id:103018 bulk water German Wadden Sea October 1999 clone GWS-K17
EU531802.1 gg_id:264753 unculturable volcanos Xinjiang mud volcano (salty) clone 285
AB189359.1 gg_id:113759 cold seep sediment clone JT75-105
AY187304.2 gg_id:108676 Geopsychrobacter electrodiphilus str. A2
EU735643.1 gg_id:329004 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
FM179908.1 gg_id:353366 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl
AY155599.1 gg_id:81506 Geothermobacter ehrlichii str. SS015
GQ249592.1 gg_id:554911 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
EF687392.1 gg_id:286079 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
AF458286.1 gg_id:77161 Mono Lake California clone
NR_026076.1 gg_id:561012 Geobacter bremensis str. Dfr1; ATCC BAA-607
AAVG01000086.1 gg_id:179082 Geobacter lovleyi str. SZ
NC_007517.1 gg_id:141183 Geobacter metallireducens str. GS-15
AY653551.1 gg_id:129581 Geobacter psychrophilus str. P11
AJ534676.1 gg_id:76599 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A
AB488058.1 gg_id:581180 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
AB486606.1 gg_id:576801 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0

NR_026407.1	575070	16.4	40.2	81.2	53.9	60.3	24.5
EU246142.1	235638	5020.6	6108.8	7148.9	3827.2	7742.6	6605.8
AY062875.1	52449	2788.5	3009.1	4101.9	3180.1	6718.4	4123.7
AJ519664.1	76391	2609.0	5071.2	1759.5	1742.8	5949.0	6783.8
AB294287.1	210461	875.1	1639.6	2138.6	1090.3	2411.4	2791.4
X79415.1	10692	3022.1	3881.3	4456.7	2083.4	2093.1	1269.6
GQ433952.1	554572	6881.3	9662.6	10929.5	7200.6	11856.6	10216.9
EU542456.1	263005	7458.3	8053.0	8523.0	7455.2	10179.4	7472.4
NR_026154.1	552396	76.3	192.4	830.3	195.1	68.1	68.3
GU180167.1	581956	4221.7	4929.8	5368.7	4879.0	6199.1	3838.4
NR_026479.1	539100	23.1	24.8	12.4	65.3	59.2	22.7
FJ638573.1	538924	7719.0	6677.6	7305.1	5638.1	6632.4	5511.5
AY280424.1	101417	7428.3	8938.6	6668.1	7246.8	9431.3	8058.4
EU386013.1	262433	2116.6	3482.3	3398.4	1401.1	3205.4	2805.2
GQ246309.1	511753	1106.2	1515.6	2234.8	1023.9	1685.9	1764.1
EU052244.1	237074	4964.8	6580.0	5597.7	5298.4	4830.6	3679.8
DQ677843.1	245056	1775.3	2075.0	3284.5	939.9	764.9	1682.0
DQ309326.1	145062	25.5	152.8	269.4	100.3	567.3	90.5
AJ441215.1	74843	2960.1	3097.6	3793.6	2170.0	3072.7	3283.2
EU052243.1	252121	2214.4	2202.4	3843.3	2212.5	1156.4	1590.4
AY187308.1	102591	5823.5	7551.6	7536.4	6406.0	8679.5	7042.1
EU617856.1	346218	14909.5	14637.9	9157.8	10991.8	15803.0	12802.8
AB355057.1	236199	8051.6	8521.4	10139.6	8696.5	9123.0	9527.2
AY998187.1	115871	16114.1	16231.4	17718.6	14310.5	18527.0	15996.8
AY515473.1	103018	8858.4	8385.5	6642.5	6625.7	7128.9	5926.6
EU531802.1	264753	27.5	141.7	69.8	48.4	217.3	26.1
AB189359.1	113759	1289.9	1825.9	3785.4	1386.9	485.9	1001.3
AY187304.2	108676	12819.8	11237.0	5237.0	9591.5	13461.6	11237.2
EU735643.1	329004	7443.7	9591.3	5880.9	5944.8	5334.2	5637.0
FM179908.1	353366	3310.4	6651.6	6594.1	3194.8	2329.7	1625.7
AY155599.1	81506	2148.8	3484.3	2955.4	3360.7	2324.6	1888.7
GQ249592.1	554911	10012.2	11106.1	9221.7	7580.9	15661.5	11248.8
EF687392.1	286079	6185.2	8024.1	11044.9	6237.0	5881.7	5992.0
AF458286.1	77161	64.4	233.1	263.2	90.2	83.1	68.0
NR_026076.1	561012	3212.5	3752.0	7117.2	4388.3	3393.0	1935.4
AAVG01000086.1	179082	3745.8	3384.7	5498.2	2358.3	4706.7	3154.0
NC_007517.1	141183	842.6	2037.0	7897.7	1605.9	1713.8	2587.6
AY653551.1	129581	631.1	992.5	6775.4	1140.9	784.6	1426.2
AJ534676.1	76599	1201.0	2338.3	2983.8	1181.9	1227.6	1380.0
AB488058.1	581180	1735.4	2261.2	4265.7	1312.0	2329.4	2740.8
AB486606.1	576801	2779.2	3682.1	4663.3	830.4	1709.1	2595.9

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NC_002939.4 gg_id:108300 Geobacter sulfurreducens str. PCA
NC_009483.1 gg_id:233864 Geobacter uraniumreducens str. Rf4
NC_008609.1 gg_id:179753 Pelobacter propionicus str. DSM 2379
AB307657.1 gg_id:262500 clay wall used Japanese traditional buildings clone R33
FJ793176.1 gg_id:532352 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB56
AJ617860.1 gg_id:109573 oxic-anoxic interphase flooded paddy soil clone D28213
AB487900.1 gg_id:590693 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
GQ487953.1 gg_id:563942 Microbial metal soil polluted heavy metals clone T7-90
EF515449.1 gg_id:222702 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24e09
FM204965.1 gg_id:569815 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
FJ461924.1 gg_id:548027 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
FJ461960.1 gg_id:557399 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AJ307942.1 gg_id:18952 derived microbial 'pearl'- community clone sipK44
AB488320.1 gg_id:576040 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
AB486133.1 gg_id:543299 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AY922116.1 gg_id:113721 farm soil clone AKYH1470
AB487641.1 gg_id:591167 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSRC
FJ461907.1 gg_id:544277 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AB486599.1 gg_id:589964 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
GQ355025.1 gg_id:555760 structure between two geochemically distinct springs Alum Rock Park spring clone M
DQ138957.1 gg_id:139194 chemical fertilizer paddy soil clone JG135
FJ269083.1 gg_id:326474 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil
GQ263990.1 gg_id:582001 Structure Simulated Level Waste Site simulated level waste site clone WC2_80
AB486446.1 gg_id:590701 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EF527427.1 gg_id:222124 Geobacter uraniumreducens str. Rf4
AY947909.1 gg_id:142841 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
FJ461957.1 gg_id:585743 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AM713386.1 gg_id:239296 Heterogeneity microorganisms sediments caused pH coal-mining lake sediment Fe(
DQ086800.1 gg_id:143335 Geobacter sp. str. CLFeRB
AB240241.1 gg_id:144252 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
EU335196.1 gg_id:242051 Changes microbial metabolic and along hydrogeochemically variable profile saturate
NR_026077.1 gg_id:552049 Geobacter pelophilus str. Dfr2; ATCC BAA-603
AB307656.1 gg_id:259279 clay wall used Japanese traditional buildings clone R40
AB234266.1 gg_id:149023 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
FJ393130.1 gg_id:358635 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel
Y19190.1 gg_id:10733 Geobacter sp. str. CdA-2
EF014495.1 gg_id:236914 Geobacter sp. G02
AB240367.1 gg_id:144809 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon
DQ354751.1 gg_id:150927 subsurface water clone MS140BH1062003ms331
CP001124.1 gg_id:312961 Geobacter bemidjiensis str. Bem
AY013644.2 gg_id:23462 sample taken downstream landfill clone BVB71 landfill

NC_002939.4	108300	216.9	425.5	1408.6	429.4	536.8	210.2
NC_009483.1	233864	2864.1	3643.0	7162.2	3572.4	1822.3	3135.4
NC_008609.1	179753	478.5	1703.3	10849.5	1182.0	1516.9	3119.9
AB307657.1	262500	425.6	744.2	8562.4	1178.1	401.6	166.9
FJ793176.1	532352	126.5	263.8	1254.9	612.3	624.7	688.6
AJ617860.1	109573	1392.4	1849.9	669.7	760.5	1835.2	1623.6
AB487900.1	590693	2528.4	3581.2	6270.9	3694.3	2811.9	2964.1
GQ487953.1	563942	133.3	265.9	1119.6	183.2	119.1	212.2
EF515449.1	222702	12983.0	12785.2	9450.7	9118.9	8999.4	7066.4
FM204965.1	569815	2665.2	2791.8	2185.0	3577.2	6546.2	4258.8
FJ461924.1	548027	3658.1	2709.6	16438.0	6245.8	4161.6	3854.9
FJ461960.1	557399	12470.1	11502.1	7718.1	9568.0	11051.8	9798.6
AJ307942.1	18952	618.7	892.9	11805.1	2039.8	142.6	456.1
AB488320.1	576040	724.7	1919.3	4958.7	836.4	1732.4	1274.8
AB486133.1	543299	740.5	2486.3	4008.8	631.5	576.3	567.8
AY922116.1	113721	145.9	321.6	1740.0	244.9	76.9	217.7
AB487641.1	591167	337.9	847.2	3072.6	1210.8	140.7	480.3
FJ461907.1	544277	1334.1	2471.2	6668.5	3017.7	396.0	932.4
AB486599.1	589964	1183.1	1140.5	6363.8	1563.1	1991.1	1322.3
GQ355025.1	555760	170.8	342.4	2940.0	588.2	233.6	69.3
DQ138957.1	139194	8005.0	5742.9	11135.5	6303.3	8084.7	7143.6
FJ269083.1	326474	12090.8	16796.0	10305.4	10550.3	12484.8	10618.4
GQ263990.1	582001	5457.6	5841.1	10229.9	4481.1	5885.3	6348.5
AB486446.1	590701	732.8	1651.5	7434.6	1025.6	1257.3	1114.1
EF527427.1	222124	126.3	353.4	2389.0	404.1	148.6	84.2
AY947909.1	142841	5917.1	8174.2	9405.9	6514.4	9430.7	8331.7
FJ461957.1	585743	17057.6	17745.8	9295.7	13635.5	15900.6	15145.6
AM713386.1	239296	11853.0	10295.2	10702.6	8974.7	12659.3	9324.6
DQ086800.1	143335	24.7	64.4	75.2	55.5	55.0	41.2
AB240241.1	144252	1972.7	2323.6	5558.0	1786.8	1251.2	590.5
EU335196.1	242051	2948.1	2814.4	3717.5	2337.4	1959.7	2115.4
NR_026077.1	552049	894.1	800.8	1435.4	631.1	930.0	904.1
AB307656.1	259279	2111.9	2581.5	3846.3	3677.0	275.9	2263.1
AB234266.1	149023	3002.0	1394.0	5516.4	2098.8	3329.8	3582.4
FJ393130.1	358635	11271.8	8539.0	8197.9	3982.4	6613.0	5387.1
Y19190.1	10733	220.9	410.8	2322.9	805.4	1607.5	1053.5
EF014495.1	236914	3012.3	3402.6	5195.8	2524.2	1406.6	1458.3
AB240367.1	144809	3100.7	3637.6	7048.4	3551.5	3920.1	3668.5
DQ354751.1	150927	1655.1	3972.4	5400.6	922.0	1651.7	835.0
CP001124.1	312961	9723.5	11568.2	6189.8	6552.4	9337.9	5945.3
AY013644.2	23462	5735.8	6409.0	8592.7	5618.1	8242.3	7972.9

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DQ145534.1 gg_id:141399 Geobacter argillaceus str. G12
DQ676355.1 gg_id:226377 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AF335183.1 gg_id:29370 Geobacter grbiciae str. TACP-5
DQ145535.1 gg_id:142149 Geobacter pickeringii str. G13
FM204949.1 gg_id:571587 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
EF515364.1 gg_id:225124 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23d10
EF527233.1 gg_id:220762 Geobacter sp. Ply1 str. PLY1
AJ009496.1 gg_id:10720 anaerobic TCB-transforming consortium clone SJA-152
Y19191.1 gg_id:10708 Geobacter sp. str. CdA-3
FJ479238.1 gg_id:593010 species richness estimates obtained nearly and simulated pyrosequencing-generated
AM713384.1 gg_id:258079 Heterogeneity microorganisms sediments caused pH coal-mining lake sediment Fe(
EF527234.1 gg_id:220531 Geobacter sp. Ply4 str. PLY4
AY395392.1 gg_id:104157 pasture soil clone EB1073
AB488092.1 gg_id:552927 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
EF515400.1 gg_id:224061 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23h09
AY737507.1 gg_id:105662 Geobacter hephaestius str. VeEG4
NR_025895.1 gg_id:543004 Geobacter metallireducens str. GS-15; ATCC 53774
AY214185.1 gg_id:82426 benzene-contaminated groundwater clone ZZ12C11
EF515282.1 gg_id:218355 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22d02
FM204997.1 gg_id:547916 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
EF515564.1 gg_id:217229 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
EU335191.1 gg_id:251985 Changes microbial metabolic and along hydrogeochemically variable profile saturate
AB239707.1 gg_id:143933 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
AY297795.1 gg_id:89444 waterlogged archaeological wood clone pACH72
EF520540.1 gg_id:231136 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-53
AY770971.1 gg_id:108346 water injection well Dagang oilfield clone W31
AF223382.1 gg_id:32027 Trichlorobacter thiogenes
EF520542.1 gg_id:229376 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-26
FM210335.1 gg_id:572312 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
EU335154.1 gg_id:244045 Changes microbial metabolic and along hydrogeochemically variable profile saturate
AB447710.1 gg_id:570781 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R
AB262721.1 gg_id:255281 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-10
EU244079.1 gg_id:356946 16SrRNA probes river Leine sediment clone sl1361
FJ478832.1 gg_id:511698 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ461926.1 gg_id:541076 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
EU134368.1 gg_id:252584 tallgrass prarie soil clone FFCH5218
EF515297.1 gg_id:223706 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22e08
EF192881.1 gg_id:202514 sediments temperate artificial lake Rapel reservoir sediment clone Rap1_22D
AY922036.1 gg_id:113772 farm soil clone AKYG597
AB186850.1 gg_id:107711 polychlorinated dioxin dechlorinating microcosm clone TSBW04
AB488109.1 gg_id:590962 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0

DQ145534.1	141399	260.3	551.0	6097.0	1022.1	87.6	54.4
DQ676355.1	226377	16045.6	13617.4	17954.6	13000.3	13003.5	12312.2
AF335183.1	29370	929.9	2315.2	8311.7	1124.2	1706.7	2163.8
DQ145535.1	142149	1141.2	1811.6	4202.3	1011.0	651.3	748.3
FM204949.1	571587	2496.8	2561.1	2148.1	3499.9	4403.8	3978.2
EF515364.1	225124	1186.0	1544.4	7859.7	906.6	569.8	885.8
EF527233.1	220762	1183.1	1907.0	2118.6	2045.0	2046.4	2788.0
AJ009496.1	10720	10755.1	10942.9	8730.5	9582.6	12786.2	10600.1
Y19191.1	10708	8845.8	10395.2	11492.4	6802.4	8084.0	5947.2
FJ479238.1	593010	2440.8	2599.4	6956.8	5325.2	1947.0	1672.0
AM713384.1	258079	428.7	639.6	9407.9	1183.4	1164.3	2117.0
EF527234.1	220531	2203.3	3497.6	5378.0	1332.5	1450.1	2130.5
AY395392.1	104157	140.6	195.2	1221.2	231.4	123.7	133.7
AB488092.1	552927	6576.8	10712.3	5947.3	6007.1	9442.0	6263.8
EF515400.1	224061	5262.5	8625.0	5721.3	4964.9	3086.3	3329.9
AY737507.1	105662	4929.4	4536.0	8225.9	2582.0	1548.5	2908.4
NR_025895.1	543004	10303.0	10728.2	9263.6	8244.9	11116.0	8338.8
AY214185.1	82426	4117.1	5574.4	6820.2	2516.0	5400.7	2877.6
EF515282.1	218355	4479.0	4951.1	7217.1	6267.9	6691.7	7756.0
FM204997.1	547916	529.7	1122.8	4083.0	1594.0	1110.0	383.0
EF515564.1	217229	3158.5	3955.8	3713.0	5029.6	6345.4	5957.7
EU335191.1	251985	2969.0	4886.6	6549.7	3129.2	5077.4	4490.7
AB239707.1	143933	11524.6	12298.7	7493.2	7351.2	11197.6	9469.4
AY297795.1	89444	294.0	512.4	8252.6	1414.0	92.3	356.2
EF520540.1	231136	1268.4	1972.8	10959.9	2360.0	1059.6	2399.1
AY770971.1	108346	776.2	1724.7	10746.3	1881.6	405.7	713.0
AF223382.1	32027	1125.6	2052.9	5084.6	1800.4	2633.9	1898.0
EF520542.1	229376	5865.5	6495.9	8727.4	5798.2	7746.6	2336.6
FM210335.1	572312	6259.7	7211.6	8039.2	6889.6	10042.1	7236.2
EU335154.1	244045	4936.0	6076.3	10266.5	5515.8	9523.0	8952.4
AB447710.1	570781	4839.4	4946.2	6249.4	3454.7	2599.5	3713.4
AB262721.1	255281	242.2	717.4	2808.0	298.2	311.4	210.6
EU244079.1	356946	1555.7	2252.5	5735.2	1151.9	1421.2	2445.5
FJ478832.1	511698	1573.2	1457.9	3284.0	2416.6	2078.9	1341.5
FJ461926.1	541076	4215.9	5035.0	7345.3	6325.8	3134.1	4623.4
EU134368.1	252584	8108.9	8281.1	8542.5	8927.5	10616.3	8363.1
EF515297.1	223706	908.2	1974.6	3912.4	1457.1	772.4	1442.6
EF192881.1	202514	293.2	343.1	6131.0	924.2	67.6	25.6
AY922036.1	113772	7379.0	6884.6	6160.0	5733.3	10745.9	9662.1
AB186850.1	107711	11600.7	10309.9	10866.5	10529.8	10935.6	8690.2
AB488109.1	590962	2630.7	2824.5	4118.3	3196.0	3527.4	2421.5

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AB486722.1 gg_id:534035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR
AY947936.1 gg_id:141881 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
AB488329.1 gg_id:535240 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
CP000142.1 gg_id:140482 Pelobacter carbinolicus str. DSM 2380
EU528245.1 gg_id:287305 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AF357914.2 gg_id:51450 Desulfuromonas michiganensis str. BRS1
U41562.1 gg_id:10667 Pelobacter venetianus
DQ647155.1 gg_id:251658 Microbial structure -temperature oil-field produced water Troll formations North Se
AB243821.1 gg_id:240641 Methods Investigate Microbial Niigata oil well clone Niigata-10
AY570613.1 gg_id:108489 biodegraded Canadian oil reservoir clone PL-27B4
AB294283.1 gg_id:215360 Microbial structure deep coal seem groundwater clone YWB14
EU328027.1 gg_id:279210 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
GU180166.1 gg_id:537907 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
AM745207.1 gg_id:293270 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
U23140.1 gg_id:10684 "Desulfuromonas acetexigens"
AB186848.1 gg_id:103899 polychlorinated dioxin dechlorinating microcosm clone TSAC13
AY185329.1 gg_id:107087 Desulfuromonas sp. clone AKS68
X70955.1 gg_id:10668 Pelobacter acetylenicus str. WoAcy1 DSM2348
GQ433929.1 gg_id:580755 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst
EU491247.1 gg_id:276607 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU134335.1 gg_id:243283 tallgrass prarie soil clone FFCH4372
EU669605.1 gg_id:329697 soil clone S11-29
GQ495396.1 gg_id:561622 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-39
EF494339.1 gg_id:223032 Nunnock River granitic landscape clone NR.1.030
EU335175.1 gg_id:243968 Changes microbial metabolic and along hydrogeochemically variable profile saturate
EU236382.1 gg_id:299505 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91H5
AF130847.1 gg_id:24509 Candidatus Entotheonella palauensis
AM697535.1 gg_id:223474 sequencing libraries indoor dust clone BF0002D046
FJ466208.1 gg_id:534885 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ479408.1 gg_id:559177 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ542849.1 gg_id:531899 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
EF516200.1 gg_id:224375 grassland soil clone FCPT594
DQ450812.1 gg_id:159853 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
AY792293.1 gg_id:119981 Humic Lake clone CrystalBog021E5
EU134440.1 gg_id:241214 tallgrass prarie soil clone FFCH11684
EF516730.1 gg_id:225970 grassland soil clone FCPP728
EF516405.1 gg_id:226410 grassland soil clone FCPT673
EU803523.1 gg_id:339137 It's all ranking aquatic Lake Gatun clone 5C231108
AJ233906.1 gg_id:10634 Cystobacter violaceus str. Cb vi34
DQ768113.1 gg_id:169959 Cystobacter minus str. DSM 14751

AB487169.1	588904	700.5	1587.0	2846.7	864.8	3844.4	3260.6
AB486722.1	534035	2512.3	2968.6	11591.7	4005.4	4412.4	5072.0
AY947936.1	141881	32.2	47.6	57.2	81.6	59.8	19.7
AB488329.1	535240	2661.0	2429.9	3745.6	689.1	147.5	730.3
CP000142.1	140482	913.7	1439.7	3140.7	1405.0	618.9	1731.4
EU528245.1	287305	1388.4	2429.2	5093.9	2735.9	1847.0	3440.4
AF357914.2	51450	5214.5	5234.3	5717.0	3644.8	4239.7	3713.0
U41562.1	10667	1581.1	2370.5	3304.1	1128.8	1024.2	2001.6
DQ647155.1	251658	2273.0	2598.9	3866.2	541.5	592.2	1237.8
AB243821.1	240641	1177.8	2767.0	3735.1	1473.3	1064.3	1947.0
AY570613.1	108489	7129.3	7867.8	8234.7	8353.3	11579.8	11697.7
AB294283.1	215360	2140.6	1939.0	2521.8	1693.2	2829.1	2854.7
EU328027.1	279210	4805.5	5105.4	6832.0	3955.4	5962.4	6143.0
GU180166.1	537907	11921.6	12735.4	11445.5	11559.9	7542.2	10536.2
AM745207.1	293270	1680.7	2269.7	5009.8	1994.8	847.5	1956.7
U23140.1	10684	3229.1	3934.3	6441.9	1463.7	1194.4	1366.2
AB186848.1	103899	3228.0	4391.4	7843.6	2771.9	4329.6	4511.7
AY185329.1	107087	5428.4	5250.4	5077.6	5077.4	3037.5	3724.9
X70955.1	10668	1194.1	1833.5	2761.2	1172.6	2305.7	967.6
GQ433929.1	580755	6105.2	7340.9	8539.9	7693.4	14503.1	10268.8
EU491247.1	276607	9949.6	10759.4	9503.3	9867.0	8234.1	9049.2
EU134335.1	243283	4749.8	4069.7	7645.3	4008.1	5079.2	6256.8
EU669605.1	329697	1299.3	1963.5	796.4	2075.2	1804.9	2697.7
GQ495396.1	561622	7294.5	6661.9	7061.1	5564.1	5376.5	10174.3
EF494339.1	223032	4797.2	5009.8	4741.5	4550.6	3470.9	5594.0
EU335175.1	243968	4895.3	6147.7	4611.4	3911.0	3614.5	4449.4
EU236382.1	299505	2686.1	3665.4	3421.3	1382.1	2213.9	2024.7
AF130847.1	24509	165.9	186.4	374.8	145.5	121.2	119.9
AM697535.1	223474	1995.2	2381.7	5074.5	3210.8	6062.0	3633.1
FJ466208.1	534885	149.0	173.4	426.2	119.8	270.7	95.7
FJ479408.1	559177	3006.8	3327.9	3974.0	2951.6	11934.7	2486.2
FJ542849.1	531899	7458.3	8332.2	13851.1	9077.7	7792.3	7094.7
EF516200.1	224375	1008.9	1205.0	2154.2	920.4	2938.7	2267.5
DQ450812.1	159853	413.7	97.6	1919.5	435.2	109.5	40.6
AY792293.1	119981	3129.5	3792.2	2774.0	1243.2	1952.9	1436.3
EU134440.1	241214	8543.0	7357.7	6968.3	6816.7	11402.6	10610.5
EF516730.1	225970	2011.9	2174.0	3502.7	2164.2	1833.6	1988.2
EF516405.1	226410	75.5	171.4	394.5	108.1	71.4	40.1
EU803523.1	339137	2777.9	6508.0	7432.7	3216.4	3156.4	4593.6
AJ233906.1	10634	1589.6	1967.2	3261.8	2440.4	886.4	1498.6
DQ768113.1	169959	1951.1	2298.1	4762.7	3465.8	1073.0	1929.9

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DQ768114.1 gg_id:172938 Cystobacter violaceus str. DSM 14727
AJ233913.1 gg_id:10629 Archangium gephyra str. Ar g2
AJ233910.1 gg_id:10626 Angiococcus disciformis str. d4
AB218222.1 gg_id:148095 Archangium gephyra str. NBRC 100087
AJ233900.1 gg_id:10630 Cystobacter ferrugineus str. Cb fe13
DQ768109.1 gg_id:168891 Cystobacter fuscus str. DSM 2262
DQ768115.1 gg_id:169963 Cystobacter velatus str. DSM 14718
AJ233897.1 gg_id:10617 Cystobacter fuscus str. Cb f6
EU263004.1 gg_id:274606 Cystobacter fuscus str. Cb9737
AJ233902.1 gg_id:10621 Cystobacter ferrugineus str. Cb fe27
AM930267.1 gg_id:251539 Melittangium lichenicola str. DSM 14877
EU262995.1 gg_id:264353 Cystobacter fuscus str. Bj41
DQ768107.1 gg_id:169848 Cystobacter armeniaca str. DSM 14710
DQ768111.1 gg_id:163670 Cystobacter miniatus str. DSM 14712
AJ970180.1 gg_id:133876 Stigmatella erecta str. DSM 16858
EU193069.1 gg_id:365027 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AJ233911.1 gg_id:10627 Angiococcus disciformis str. d6
AJ233905.1 gg_id:10633 Cystobacter violaceus str. Cb vi29
AJ233944.1 gg_id:10652 Polyangium vitellinum str. Pl vt1
EF108312.1 gg_id:180118 Haliangium ochraceum str. GS1
AB062751.1 gg_id:38718 Haliangium tepidum
EU134537.1 gg_id:236984 tallgrass prarie soil clone FFCH18685
FJ712545.1 gg_id:530479 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AB286567.1 gg_id:204372 Reducing production and domination comamonadaceae reducing oxygen supply was
GQ264394.1 gg_id:574674 Structure Simulated Level Waste Site simulated level waste site clone WW2_84
AM072418.1 gg_id:137564 uranium mining waste pile soil clone JG35-2-JT67
EF018702.1 gg_id:204556 aspen rhizosphere clone Amb_16S_999
FJ479136.1 gg_id:578408 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ396851.1 gg_id:566634 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EU134437.1 gg_id:242508 tallgrass prarie soil clone FFCH11506
EU134439.1 gg_id:236963 tallgrass prarie soil clone FFCH11594
EU676441.1 gg_id:300085 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
AY921676.1 gg_id:113324 farm soil clone AKYH1423
AJ518792.1 gg_id:76933 uranium mining waste pile clone JG37-AG-33 proteobacterium
AJ519631.1 gg_id:74929 uranium mill tailings soil clone Sh765B-TzT-42
EU617834.1 gg_id:333636 Seasonal variation microbial Yel Sea sediment clone C13S-30
EF516060.1 gg_id:217328 grassland soil clone FCPP560
EU925860.1 gg_id:353947 sediments sediment station DBS1 northern Bering Sea clone 061F22
AM490754.1 gg_id:542734 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
DQ395973.1 gg_id:152024 deep-sea octacoral clone ctg_CGOGA72
EU617837.1 gg_id:313196 Seasonal variation microbial Yel Sea sediment clone D13S-10

DQ768114.1	172938	2919.1	3403.0	6249.0	5054.9	1700.7	2611.5
AJ233913.1	10629	2385.6	2818.8	4904.0	3714.0	756.3	1694.3
AJ233910.1	10626	1653.9	1721.8	4170.5	2797.2	1333.4	1709.9
AB218222.1	148095	1708.1	2099.3	2985.6	2080.8	705.0	1625.4
AJ233900.1	10630	1622.7	2324.2	3390.6	2121.1	734.5	1836.1
DQ768109.1	168891	2327.7	2584.0	6562.5	2827.2	2290.6	2444.2
DQ768115.1	169963	1096.4	2085.9	5695.1	1372.5	1222.3	1745.3
AJ233897.1	10617	1083.1	2136.5	6626.4	1891.7	3652.4	2439.6
EU263004.1	274606	1036.0	2053.9	6279.4	1539.7	664.3	1861.0
AJ233902.1	10621	1328.5	2429.8	6991.3	2535.4	3777.2	2727.9
AM930267.1	251539	1543.4	2457.6	7255.7	2637.5	3803.6	2749.0
EU262995.1	264353	2369.8	2966.8	7839.9	2503.2	2288.2	2693.9
DQ768107.1	169848	1225.1	2170.0	6077.1	2164.7	2072.4	2227.3
DQ768111.1	163670	439.8	1116.7	4312.1	1331.0	415.3	1121.2
AJ970180.1	133876	2320.9	2669.9	7543.0	4980.6	1676.1	2953.9
EU193069.1	365027	1389.3	1909.0	3912.7	1459.1	464.2	1402.8
AJ233911.1	10627	83.5	208.8	1499.8	347.1	161.7	279.6
AJ233905.1	10633	705.0	796.0	3697.0	1965.9	324.7	866.0
AJ233944.1	10652	2485.5	3012.7	3757.9	2074.6	3181.5	3789.5
EF108312.1	180118	35.1	61.9	431.3	76.3	69.7	45.1
AB062751.1	38718	73.8	138.7	300.6	115.5	253.1	199.3
EU134537.1	236984	4490.6	3998.1	5260.1	5252.1	3677.8	5068.8
FJ712545.1	530479	2511.6	3139.8	3483.5	3982.2	1660.1	3224.2
AB286567.1	204372	1823.9	2123.5	4060.5	1801.5	2145.2	3285.4
GQ264394.1	574674	2018.7	1889.4	4409.9	1095.6	721.3	1745.8
AM072418.1	137564	9158.9	9050.2	6555.0	8870.5	13212.0	11469.5
EF018702.1	204556	3047.2	3956.2	5639.4	3886.2	4046.4	3409.2
FJ479136.1	578408	6994.8	9022.5	8903.4	6118.1	8807.0	9345.9
GQ396851.1	566634	1205.7	2098.0	4138.1	4861.6	1421.5	2892.1
EU134437.1	242508	14908.4	15840.7	20417.8	13133.1	13842.5	14658.8
EU134439.1	236963	6258.2	5656.6	9945.2	5337.6	6163.3	4915.3
EU676441.1	300085	81.2	134.4	1035.8	97.1	153.5	200.5
AY921676.1	113324	87.0	93.0	127.2	117.5	137.9	62.9
AJ518792.1	76933	66.3	85.7	239.1	84.7	79.8	51.8
AJ519631.1	74929	1758.4	1987.1	4171.4	2356.7	2983.6	2026.4
EU617834.1	333636	3429.0	2554.4	2810.0	3505.0	1550.0	1354.9
EF516060.1	217328	3883.1	5092.3	6573.2	4570.5	3862.0	3221.3
EU925860.1	353947	9460.7	9775.0	14286.8	8457.7	12389.6	10821.5
AM490754.1	542734	2478.0	3159.1	5221.2	3828.7	3023.6	4165.7
DQ395973.1	152024	728.3	459.2	1005.5	1033.4	223.2	283.7
EU617837.1	313196	532.1	748.1	3857.9	2046.6	2005.1	1955.1

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DQ640732.1 gg_id:228460 full-scale EBPR sludge clone Skagen129
AY922085.1 gg_id:114341 farm soil clone AKYG989
EU134548.1 gg_id:246356 tallgrass prarie soil clone FFCH2604
EU335231.1 gg_id:256412 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AY862012.1 gg_id:112562 Queens Laundry berry community clone QLBB011
FJ748771.1 gg_id:578632 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar
EF515967.1 gg_id:224129 grassland soil clone FCPO510
EF516802.1 gg_id:221219 grassland soil clone FCPS608
EF516477.1 gg_id:218069 grassland soil clone FCPO701
EU617835.1 gg_id:345106 Seasonal variation microbial Yel Sea sediment clone D13S-24
EF999387.1 gg_id:244765 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn
DQ811794.1 gg_id:173727 mangrove soil clone MSB-3B11
FJ466420.1 gg_id:566988 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU652608.1 gg_id:279253 Seasonal variation microbial Yel Sea sediment clone B8S-115
GU119139.1 gg_id:570059 Threatened Corals Provide Microbial Habitats clone Past_J10
AB286332.1 gg_id:204177 Reducing production and domination comamonadaceae reducing oxygen supply was
AY622263.1 gg_id:99343 subsurface soil clone B-BK96
FM253665.1 gg_id:305498 Rock gold mine unusually microbial biofilm clone F04-2
FJ478686.1 gg_id:570453 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ478958.1 gg_id:543753 species richness estimates obtained nearly and simulated pyrosequencing-generated
AJ241020.1 gg_id:10682 Norway:(Svalbard)Hornsund clone Sva0679
GU208498.1 gg_id:592792 Study on Sediment Dongping Lake sediment clone Shf1-5
FJ466408.1 gg_id:548168 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AJ576419.1 gg_id:102303 midgut homogenate Pachnoda ephippiata larva clone PeM65
EF580975.1 gg_id:277714 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1
EF999354.1 gg_id:244128 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm
AY921674.1 gg_id:113379 farm soil clone AKYH1085
EU445232.1 gg_id:563875 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R84
GU118929.1 gg_id:546642 Threatened Corals Provide Microbial Habitats clone Past_O02
DQ906778.1 gg_id:254611 Oman subsurface soil clone 2A-7
GQ264118.1 gg_id:551080 Structure Simulated Level Waste Site simulated level waste site clone WC3_53
EU617833.1 gg_id:332464 Seasonal variation microbial Yel Sea sediment clone D13S-2
AM997778.1 gg_id:572137 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU134286.1 gg_id:256241 tallgrass prarie soil clone FFCH3218
EU134430.1 gg_id:239367 tallgrass prarie soil clone FFCH10899
AY921878.1 gg_id:113228 farm soil clone AKYH1170
EF580944.1 gg_id:278622 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6
EF019351.1 gg_id:207878 aspen rhizosphere clone Elev_16S_566
EU861852.1 gg_id:345643 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog
NC_009675.1 gg_id:250283 Anaeromyxobacter sp. str. Fw109-5

AB294333.1	209489	3067.8	3624.4	6839.2	4124.1	3593.4	4137.6
DQ640732.1	228460	64.0	211.0	762.8	179.5	148.9	171.2
AY922085.1	114341	4364.5	2141.9	4137.5	3726.5	2331.5	3475.2
EU134548.1	246356	2521.0	4348.8	8048.9	2675.5	3913.4	5970.1
EU335231.1	256412	654.2	1095.4	2246.1	664.9	1081.6	1210.6
AY862012.1	112562	281.1	699.0	1804.6	342.8	1066.4	935.8
FJ748771.1	578632	6527.0	6004.3	5741.8	7691.3	9318.7	9928.9
EF515967.1	224129	87.1	167.2	562.5	105.2	73.2	153.4
EF516802.1	221219	20.6	25.6	43.7	58.6	71.1	29.8
EF516477.1	218069	40.0	82.0	424.0	102.2	117.0	144.5
EU617835.1	345106	3891.7	5380.5	10064.8	2551.4	4398.0	6369.7
EF999387.1	244765	14366.8	14387.4	11854.8	14286.0	13861.9	14620.4
DQ811794.1	173727	3203.4	2998.0	3647.5	3801.4	5016.3	4794.0
FJ466420.1	566988	51.6	55.3	199.8	122.1	92.0	68.5
EU652608.1	279253	1333.3	1528.8	2026.6	2097.9	563.7	1621.8
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AB286332.1	204177	1029.0	1409.0	2145.6	628.6	259.9	361.3
AY622263.1	99343	721.1	1585.1	7793.9	1285.9	2161.8	2431.1
FM253665.1	305498	5984.2	6960.9	3835.1	7249.0	6214.6	6975.1
FJ478686.1	570453	6192.7	6729.6	7173.7	3530.4	5716.5	5560.3
FJ478958.1	543753	3029.2	4114.9	13185.6	3717.6	5673.8	6622.4
AJ241020.1	10682	11130.7	11474.4	12172.0	13278.9	14877.4	14152.1
GU208498.1	592792	817.5	1071.3	1992.8	546.6	1484.2	2462.0
FJ466408.1	548168	2749.4	4495.6	3818.7	3655.7	3587.8	3632.2
AJ576419.1	102303	521.2	1147.0	3007.4	567.8	1055.3	1483.4
EF580975.1	277714	2829.2	3690.5	4183.1	4312.5	3687.1	2466.7
EF999354.1	244128	833.9	1076.9	4077.6	1346.4	1881.3	1474.6
AY921674.1	113379	860.7	1507.2	3070.7	1290.4	758.8	2402.7
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GQ397088.1 gg_id:532843 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EU134349.1 gg_id:236268 tallgrass prarie soil clone FFCH6412
FJ190071.1 gg_id:335745 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s
FJ190063.1 gg_id:353729 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s
EU134508.1 gg_id:241430 tallgrass prarie soil clone FFCH17129
AM162453.1 gg_id:151071 and situ identification acidic sphagnum peat bog clone B88
FJ190066.1 gg_id:324580 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s
EU331407.1 gg_id:247762 Anaeromyxobacter dehalogenans str. DCP15
FJ190072.1 gg_id:317365 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s
GQ402739.1 gg_id:579915 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
GQ402712.1 gg_id:582110 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
EU307086.1 gg_id:249072 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AY921809.1 gg_id:113159 farm soil clone AKYG886
EF520536.1 gg_id:234490 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-17
AF382397.1 gg_id:24157 Anaeromyxobacter dehalogenans str. 2CP-5
FJ190062.1 gg_id:312494 Anaeromyxobacter dehalogenans str. FRC-W
AB486683.1 gg_id:571531 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
AJ233915.1 gg_id:10592 Myxococcus coralloides str. Cc c806
GU139156.1 gg_id:587638 Corallococcus macrosporus str. HBUM91004
EU263003.1 gg_id:259044 Corallococcus coralloides str. 0185-2
EU263002.1 gg_id:263917 Corallococcus coralloides str. 0198-2
GQ246607.1 gg_id:550449 Corallococcus exiguus str. HBUM94202
AJ233931.1 gg_id:10589 Corallococcus exiguus str. Cc e12b
AM930268.1 gg_id:247897 Melittangium lichenicola str. ATCC 25944
AJ811614.1 gg_id:106360 Corallococcus coralloides str. DSM 51301
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AY724799.1 gg_id:105036 Myxococcus xanthus str. UCDaV16
AY072737.1 gg_id:17656 Myxococcus macrosporus str. 125-10-3
AY072740.1 gg_id:21317 Myxococcus macrosporus str. 125-10-1
AY724798.1 gg_id:104894 Myxococcus xanthus str. UCDaV5
EU271853.1 gg_id:251509 Myxococcus stipitatus str. KYC1101
GQ246570.1 gg_id:590399 Myxococcus stipitatus str. HBUM92079
EU262651.1 gg_id:243378 Myxococcus fulvus str. KYC1136
EU262655.1 gg_id:237067 Myxococcus fulvus str. KYC1198

GQ397088.1	532843	2038.5	2726.4	4254.1	565.2	533.9	1261.1
EU134349.1	236268	1988.6	2694.5	3800.8	2156.1	3627.8	2852.8
FJ190071.1	335745	5440.0	8399.3	6684.0	5945.8	8724.1	8380.6
FJ190063.1	353729	5690.0	4939.3	9478.8	5911.8	5354.8	7396.4
EU134508.1	241430	3213.0	3523.1	5204.7	4371.3	2318.1	1612.7
AM162453.1	151071	2828.3	3333.7	7222.5	2866.4	2714.9	2777.8
FJ190066.1	324580	7408.4	7909.3	10440.6	6252.8	8120.8	9820.3
EU331407.1	247762	8510.9	9357.8	13560.1	8821.2	11446.8	9678.0
FJ190072.1	317365	5706.0	6021.2	10325.6	5223.9	3140.3	5609.1
GQ402739.1	579915	4530.5	6136.1	11688.2	5526.3	8874.4	6972.0
GQ402712.1	582110	2704.8	5181.2	9823.2	2087.0	4003.1	3910.0
EU307086.1	249072	1658.6	2487.4	8607.1	2856.9	1590.0	2298.0
AY921809.1	113159	45.6	168.2	212.8	83.6	50.5	44.8
EF520536.1	234490	727.2	2080.1	7077.2	938.1	619.2	2635.5
AF382397.1	24157	1001.4	1384.8	4540.6	1513.0	890.3	1577.3
FJ190062.1	312494	275.0	809.5	3432.9	976.7	713.3	914.4
AB486683.1	571531	5140.8	7397.4	7391.7	6197.2	7268.9	8260.8
AJ233915.1	10592	4111.2	4410.0	7821.5	5376.7	5481.9	5390.5
GU139156.1	587638	5134.9	5970.8	10026.0	6498.2	7950.2	6865.1
EU263003.1	259044	4103.5	4823.7	5663.0	4950.3	2935.0	3585.9
EU263002.1	263917	4714.2	5154.2	8588.8	6351.4	6625.3	6741.3
GQ246607.1	550449	2862.2	3266.4	4251.3	3037.9	1661.3	2172.2
AJ233931.1	10589	4015.9	4333.9	7756.4	5318.3	5388.3	5184.0
AM930268.1	247897	3429.7	3614.1	9125.4	5814.1	5384.8	3969.7
AJ811614.1	106360	4234.8	4640.1	5470.3	4715.7	3160.6	3412.8
AJ811612.1	106050	2362.0	2944.7	3790.2	2791.0	994.8	2053.4
AJ811595.1	105288	8668.5	8820.5	10570.9	10044.8	11250.2	10962.5
EU262999.1	265680	3350.3	3552.9	5161.2	4118.7	3584.0	3303.5
AJ811593.1	104972	3688.4	3995.1	7277.1	4584.5	5939.5	5074.7
AJ811601.1	100844	4270.0	4647.6	5467.0	4734.2	3636.2	4026.8
AJ811604.1	101327	2863.1	3180.2	3998.9	3032.1	1639.0	1999.3
AJ811615.1	106528	2798.4	3585.3	4428.2	3559.5	1447.7	2674.5
AY724800.1	99811	17143.9	18099.8	19801.0	13708.6	17032.9	15437.8
AY724799.1	105036	12051.4	13875.5	14573.1	13090.4	15034.0	13143.5
AY072737.1	17656	6644.7	7566.5	10916.8	5519.7	8703.6	8831.4
AY072740.1	21317	3725.0	5037.6	4251.9	1741.6	4741.2	7672.6
AY724798.1	104894	3605.7	4118.1	7253.2	4798.3	3113.5	3886.2
EU271853.1	251509	6828.3	7602.5	12724.8	7475.5	7745.6	8046.2
GQ246570.1	590399	5282.3	6145.8	8626.3	5474.6	3282.9	4812.4
EU262651.1	243378	4178.2	4963.6	6453.1	5424.9	2961.5	4627.5
EU262655.1	237067	1732.7	1989.4	2694.2	2429.6	1990.1	2381.4

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AJ233922.1 gg_id:10607 Myxococcus stipitatus str. Mx s33
AB218209.1 gg_id:150276 Myxococcus fulvus str. NBRC 100070
GU139153.1 gg_id:579552 Myxococcus stipitatus str. HBUM93501
AJ233929.1 gg_id:10614 Myxococcus xanthus str. DSM 435 (Mx x1)
GQ246531.1 gg_id:576354 Myxococcus virescens str. HBUM93351
AJ233927.1 gg_id:10612 Myxococcus virescens str. Mx v1
AJ233909.1 gg_id:10600 Angiococcus disciformis str. d1
EU262997.1 gg_id:276309 Myxococcus macrosporus str. Myxo9736
DQ768123.1 gg_id:163033 Pyxicoccus fallax str. DSM 14698
GQ246547.1 gg_id:579922 Corallococcus macrosporus str. HBUM93406
GQ246552.1 gg_id:534207 Corallococcus macrosporus str. HBUM93407
GU139157.1 gg_id:589401 Myxococcus virescens str. HBUM91069
AJ233930.1 gg_id:10615 Myxococcus xanthus str. Mx x132
AJ811621.1 gg_id:102087 Corallococcus coralloides str. DSM 52496
GQ246541.1 gg_id:539091 Myxococcus virescens str. HBUM93307
EU262992.1 gg_id:277585 Myxococcus fulvus str. 0189-5
GQ246525.1 gg_id:540091 Myxococcus fulvus str. HBUM93175
AJ233917.1 gg_id:10602 Myxococcus fulvus str. Mx f2
AJ811622.1 gg_id:102241 Corallococcus coralloides str. DSM 52498
AJ233920.1 gg_id:10605 Myxococcus macrosporus str. Cc m7
AY724797.1 gg_id:104738 Myxococcus xanthus str. UCDaV1
AJ233925.1 gg_id:10610 Myxococcus virescens str. Mx v2
EU158297.1 gg_id:247490 Myxococcus sp. str. HBUM 91040
GQ246558.1 gg_id:532677 Myxococcus fulvus str. HBUM93132
AF280855.1 gg_id:73433 bioreactor clone mle1-22
EU283398.1 gg_id:253563 consecutively aerated submerged treating domestic wastewater activated sludge m
ABCS01000137.1 gg_id:235635 Plesiocystis pacifica str. SIR-1
EU134550.1 gg_id:256957 tallgrass prarie soil clone FFCH2652
AY921891.1 gg_id:135973 farm soil clone AKYH963
FJ152686.1 gg_id:304479 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
EU050860.1 gg_id:245344 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_05_87
CU466781.1 gg_id:327106 Evry wastewater treatment plant anoxic basin clone
FJ203639.1 gg_id:313265 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
DQ298325.1 gg_id:154699 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
AB252740.1 gg_id:152915 Antimicrobial Cyclic Depsipeptides SMH-27-4A coastal soil
AM997796.1 gg_id:546538 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU236309.1 gg_id:298699 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a2H2
AJ233941.1 gg_id:10642 Chondromyces robustus str. Cm a22
NR_025346.1 gg_id:565046 Chondromyces robustus str. Cm a13; DSM 14608
DQ491070.1 gg_id:170538 Chondromyces pediculatus str. BICC 8609

GQ246569.1	589601	5227.0	5457.1	7998.7	5380.4	2922.8	4048.1
AJ233922.1	10607	6297.1	7059.3	12821.4	8815.5	7889.3	8459.2
AB218209.1	150276	6130.5	7038.7	10636.4	8149.6	7896.4	8721.2
GU139153.1	579552	6451.6	7416.3	12423.9	9057.8	8060.8	8521.2
AJ233929.1	10614	6397.1	7908.1	11197.9	8427.7	10252.7	12616.4
GQ246531.1	576354	3986.5	4856.5	6322.4	4552.5	2568.3	3703.3
AJ233927.1	10612	4316.3	5315.6	5575.4	4878.8	3638.7	5266.8
AJ233909.1	10600	6876.6	7529.9	11344.8	7330.6	7147.2	7526.1
EU262997.1	276309	6877.4	7443.7	11075.6	7324.8	7125.0	7341.7
DQ768123.1	163033	2195.6	3289.7	6112.4	2774.7	1746.5	2848.1
GQ246547.1	579922	3583.2	4393.2	5437.1	4626.6	2902.4	4723.8
GQ246552.1	534207	7473.5	8422.4	14084.7	7355.6	6522.5	6663.2
GU139157.1	589401	6611.4	7067.6	9668.1	6509.9	5797.1	6697.4
AJ233930.1	10615	4676.3	5877.0	7967.6	5688.7	7684.6	9169.9
AJ811621.1	102087	4583.0	5682.8	7288.7	4436.3	2477.0	3799.0
GQ246541.1	539091	6114.5	7019.5	8854.0	6268.6	5083.9	6694.5
EU262992.1	277585	3578.9	4463.8	7105.7	4798.7	5044.3	5822.5
GQ246525.1	540091	8378.2	9034.4	9858.3	11240.6	8356.0	9240.6
AJ233917.1	10602	5514.1	5984.3	6063.8	6192.9	4928.2	5725.1
AJ811622.1	102241	6839.1	7667.3	12257.3	7487.0	7735.6	8009.9
AJ233920.1	10605	5735.3	6477.3	7912.7	5553.8	3614.4	4813.3
AY724797.1	104738	7790.0	8280.0	8555.9	5350.0	4560.6	7530.1
AJ233925.1	10610	3937.5	4953.2	6148.0	3275.3	2488.7	3322.4
EU158297.1	247490	7307.6	8070.8	6137.5	8745.1	8918.3	8967.8
GQ246558.1	532677	3909.1	4708.3	9586.7	5671.2	5039.7	4945.9
AF280855.1	73433	32.0	36.7	175.6	68.6	64.1	34.8
EU283398.1	253563	5624.0	6470.0	7976.4	7036.4	8391.4	7548.5
ABCS01000137.1	235635	2497.4	3430.2	5379.9	2146.3	3561.9	5301.1
EU134550.1	256957	3725.6	5531.3	11831.2	4781.4	10408.0	9186.4
AY921891.1	135973	289.0	512.9	395.9	256.1	128.6	354.8
FJ152686.1	304479	8193.1	7631.5	6337.4	10445.9	11478.6	10586.2
EU050860.1	245344	6794.5	6923.3	9548.4	7220.8	10431.0	11023.3
CU466781.1	327106	8727.8	8654.8	9780.2	11778.6	7837.8	11061.8
FJ203639.1	313265	3212.4	2387.7	3361.6	3517.6	3387.7	3950.3
DQ298325.1	154699	5494.1	7026.2	6846.5	4397.5	9909.2	9206.0
AB252740.1	152915	36.1	111.5	36.0	137.6	121.7	119.7
AM997796.1	546538	3595.9	4132.8	4540.2	3807.0	4893.7	4238.9
EU236309.1	298699	2198.5	2612.3	5838.3	4099.0	2925.4	5914.5
AJ233941.1	10642	367.9	981.9	4166.5	631.9	1413.4	1423.9
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FJ176772.1 gg_id:367282 Chondromyces crocatus str. KYC2823
AJ233943.1 gg_id:10645 Polyangium thaxteri str. Pl t3
AJ233938.1 gg_id:10639 Chondromyces apiculatus str. Cm a14
AY079453.1 gg_id:29731 Polyangium cellulosum str. So0089-1
AF387627.1 gg_id:26373 Polyangium cellulosum str. 9741
EU240490.1 gg_id:277159 Sorangium cellulosum str. So0184-1
FJ479176.1 gg_id:580635 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY921933.1 gg_id:113748 farm soil clone AKYG909
EU193074.1 gg_id:369028 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU881272.1 gg_id:355920 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
EU134398.1 gg_id:257391 tallgrass prarie soil clone FFCH6364
FJ479473.1 gg_id:579806 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ295908.1 gg_id:145144 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e
FJ660562.1 gg_id:551380 Correlation functional stability and dynamics full-scale wastewater treatment plant a
EF516308.1 gg_id:218711 grassland soil clone FCPO632
AJ617907.1 gg_id:109755 oxic-anoxic interphase flooded paddy soil clone D142119
EU134486.1 gg_id:245900 tallgrass prarie soil clone FFCH15612
FJ478737.1 gg_id:535402 species richness estimates obtained nearly and simulated pyrosequencing-generated
AJ833647.1 gg_id:108677 Byssophaga cruenta str. c2 = DSM 14553
AY493915.1 gg_id:136914 Fingerprinting aggregates soil clone 604
AJ233948.1 gg_id:10657 Myxococcales str. NOSO-1
AM490752.1 gg_id:588131 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
EU104167.1 gg_id:347524 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU979074.1 gg_id:326414 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
AF280858.1 gg_id:71817 bioreactor clone mle1-29
EF018417.1 gg_id:203878 aspen rhizosphere clone Amb_16S_1034
AB238772.1 gg_id:146819 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-009
EF580966.1 gg_id:278697 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1
EF112185.1 gg_id:187653 Stigmatella koreensis str. KYC-1019
EU134339.1 gg_id:240506 tallgrass prarie soil clone FFCH3210
EU134451.1 gg_id:250244 tallgrass prarie soil clone FFCH12289
EU134540.1 gg_id:237206 tallgrass prarie soil clone FFCH18737
FJ671175.1 gg_id:511742 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY725263.1 gg_id:102557 decayed velvetleaf seed clone S1-4-CL5
DQ768124.1 gg_id:170014 Hyalangium minutum str. DSM 14724
DQ129589.1 gg_id:137984 microarray level air two cities Texas urban aerosol clone AKIW811
AM697153.1 gg_id:221410 sequencing libraries indoor dust clone BF0002B103
GQ007850.1 gg_id:501815 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ152674.1 gg_id:336745 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
GQ264111.1 gg_id:568834 Structure Simulated Level Waste Site simulated level waste site clone WC3_40
DQ768110.1 gg_id:172129 Cystobacter gracilis str. DSM 14753

FJ176772.1	367282	2804.0	3675.8	7688.3	3697.9	4272.8	5525.3
AJ233943.1	10645	3433.5	3698.1	6165.2	5557.2	2303.4	4007.2
AJ233938.1	10639	2402.2	2218.8	4494.8	3618.3	3288.5	3601.0
AY079453.1	29731	9211.1	8613.4	9765.8	7954.7	7124.2	6315.9
AF387627.1	26373	10216.2	11847.4	8028.4	9680.2	11032.8	10445.5
EU240490.1	277159	56.3	240.0	1240.6	164.9	119.3	273.5
FJ479176.1	580635	185.4	467.2	2388.8	232.9	133.7	227.6
AY921933.1	113748	885.2	952.2	2563.9	574.4	552.8	1232.0
EU193074.1	369028	114.9	329.6	2529.8	142.7	141.1	155.2
EU881272.1	355920	3664.6	4256.8	7253.4	4304.6	6099.0	7173.5
EU134398.1	257391	134.9	311.3	1712.5	230.4	143.2	426.3
FJ479473.1	579806	197.9	41.2	686.9	168.7	177.7	219.1
DQ295908.1	145144	495.0	769.8	2714.3	519.6	737.0	596.1
FJ660562.1	551380	1945.2	2148.0	2873.2	2324.2	712.3	1581.7
EF516308.1	218711	18.0	31.4	75.0	50.8	56.2	17.7
AJ617907.1	109755	2034.0	1917.6	3035.7	3198.0	850.5	1764.8
EU134486.1	245900	36.9	118.6	1416.2	80.5	96.8	157.8
FJ478737.1	535402	1433.1	1927.9	5573.5	1654.8	3016.3	4110.3
AJ833647.1	108677	261.1	492.2	1160.5	332.2	167.5	325.2
AY493915.1	136914	1589.6	1229.4	610.2	4428.1	279.1	307.4
AJ233948.1	10657	149.0	127.4	300.9	103.5	110.0	56.3
AM490752.1	588131	1261.8	1200.6	4016.5	500.1	1748.9	1371.4
EU104167.1	347524	336.7	502.5	2372.6	367.8	1074.7	1670.9
EU979074.1	326414	2402.0	1752.8	1730.8	972.7	1003.8	963.7
AF280858.1	71817	10.7	83.8	16.7	50.2	40.9	8.7
EF018417.1	203878	240.1	579.6	2078.9	239.4	498.2	261.6
AB238772.1	146819	70.4	118.8	158.9	91.7	141.0	86.5
EF580966.1	278697	513.3	747.9	1377.7	1123.0	530.0	569.2
EF112185.1	187653	1155.9	1849.4	4377.7	2394.8	722.9	1926.2
EU134339.1	240506	5866.3	7267.5	10632.7	6312.4	5329.5	5329.0
EU134451.1	250244	2482.6	3589.2	4910.6	3090.1	3983.5	5879.8
EU134540.1	237206	6989.6	6852.9	10194.5	7778.5	6100.7	8498.5
FJ671175.1	511742	2839.2	3626.0	10399.4	5382.0	5168.6	3909.8
AY725263.1	102557	320.8	747.2	7277.8	675.7	385.6	428.9
DQ768124.1	170014	25.4	27.8	36.2	59.4	56.9	26.2
DQ129589.1	137984	41.4	73.3	103.6	63.1	66.9	28.6
AM697153.1	221410	869.9	1245.1	2960.1	484.5	340.0	831.1
GQ007850.1	501815	14537.0	11234.8	10554.2	10912.0	14532.1	12709.7
FJ152674.1	336745	1682.6	2435.1	9459.6	3661.9	2424.3	2525.2
GQ264111.1	568834	308.9	1395.1	2736.9	330.2	170.3	796.4
DQ768110.1	172129	144.4	459.2	2190.5	271.2	136.3	238.7

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GQ007729.1 gg_id:501937 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
FM209347.1 gg_id:575313 Microbial Negev desert s sand soil clone 110
EU015103.1 gg_id:236994 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
EF019208.1 gg_id:203689 aspen rhizosphere clone Amb_16S_1894
EU202851.1 gg_id:326656 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ479195.1 gg_id:543094 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ109933.1 gg_id:144097 Sulfate-reducing mats: Changing paradigms new discoveries salt pond nonlithifying
EF516185.1 gg_id:220256 grassland soil clone FCPN515
EU134536.1 gg_id:240725 tallgrass prarie soil clone FFCH18580
EU385735.1 gg_id:268363 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU386034.1 gg_id:274528 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EF574444.1 gg_id:232196 site S25 near Coco's Island marine clone S25_788
GQ402637.1 gg_id:580197 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ228369.1 gg_id:141905 microbial compositions two subglacial possible role microbes chemical weathering p
AM490753.1 gg_id:576469 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
EF516312.1 gg_id:218567 grassland soil clone FCPT531
FJ624903.1 gg_id:545917 Influence lead contamination on boreal pine forest soil clone HF_C_30
EU669621.1 gg_id:331980 soil clone S22-10
GQ097382.1 gg_id:392302 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
EU193067.1 gg_id:368706 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AY922068.1 gg_id:113261 farm soil clone AKYG817
EF516830.1 gg_id:219369 grassland soil clone FCPP483
DQ676313.1 gg_id:226704 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AY395395.1 gg_id:104624 pasture soil clone EB1076
FM872981.1 gg_id:360433 occupant source house floor dust clone FB02E03
GQ246391.1 gg_id:535730 Temporal and spatial China North Yel Sea sediments clone Cm1-54
GQ357027.1 gg_id:545451 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_
FJ264600.1 gg_id:353586 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
DQ334667.1 gg_id:199082 Impact heavy metals on sediments pristine marine sediment clone IF-8-27
DQ334608.1 gg_id:188421 Impact metals on sediments heavy metal polluted marine sediment clone HB1-42-2
EF125390.1 gg_id:195498 soil naked tidal flat sediment near mangrove clone MSB-1B2
EU617839.1 gg_id:307096 Seasonal variation microbial Yel Sea sediment clone C13S-53
AY225608.1 gg_id:98504 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-60
EF126277.1 gg_id:259881 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph
AM936555.1 gg_id:554552 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU193070.1 gg_id:368942 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
GQ111138.1 gg_id:380727 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU134492.1 gg_id:244127 tallgrass prarie soil clone FFCH16240
FM872766.1 gg_id:364646 occupant source house floor dust clone FB01F04
AY922176.1 gg_id:114327 farm soil clone AKYH967
EF020038.1 gg_id:208701 aspen rhizosphere clone Elev_16S_1435

GQ007729.1	501937	7255.7	7087.8	8861.2	6275.6	5748.8	6443.6
FM209347.1	575313	3323.6	2486.1	9791.0	5162.8	3318.2	4855.4
EU015103.1	236994	1959.6	2578.1	5327.5	2308.4	2705.9	3281.9
EF019208.1	203689	5830.9	6332.8	7895.9	7275.3	5678.7	6159.3
EU202851.1	326656	70.0	281.9	1434.4	203.4	218.1	317.7
FJ479195.1	543094	1544.9	2314.8	5887.1	2226.6	1572.1	2172.3
DQ109933.1	144097	4866.0	6092.9	5671.9	5868.3	8891.2	8429.0
EF516185.1	220256	42.1	118.6	934.4	94.3	81.6	62.0
EU134536.1	240725	9409.3	9388.4	8144.7	8477.6	10752.6	10175.0
EU385735.1	268363	896.8	1276.6	4171.8	1606.3	447.9	1142.2
EU386034.1	274528	4425.8	4429.1	6632.9	5730.2	3015.0	5322.0
EF574444.1	232196	64.9	118.2	336.1	177.1	214.8	164.4
GQ402637.1	580197	4289.7	5958.1	7471.6	3261.4	7414.4	5301.8
DQ228369.1	141905	255.9	257.9	1097.1	112.5	116.5	124.2
AM490753.1	576469	3969.4	3603.2	6677.8	2181.5	3606.9	3671.3
EF516312.1	218567	89.0	322.5	3383.2	188.7	218.8	348.1
FJ624903.1	545917	542.7	1013.3	3466.3	907.0	1898.9	1360.9
EU669621.1	331980	4577.0	4545.8	5622.3	3648.2	4008.4	5375.2
GQ097382.1	392302	4508.9	4934.0	5966.6	3739.2	5312.5	4847.9
EU193067.1	368706	376.1	811.6	5138.4	470.4	1039.8	799.8
AY922068.1	113261	3545.4	4143.1	9965.0	5377.1	5408.3	6236.0
EF516830.1	219369	31.1	177.1	382.9	99.6	76.6	53.1
DQ676313.1	226704	63.0	165.8	872.6	203.9	109.3	265.9
AY395395.1	104624	214.0	441.2	3086.0	273.8	342.5	676.9
FM872981.1	360433	644.4	693.4	2547.7	395.1	630.8	576.4
GQ246391.1	535730	5996.4	8044.1	7525.6	5684.5	5320.3	6100.1
GQ357027.1	545451	9050.4	9490.9	8682.4	9697.2	11971.7	10880.1
FJ264600.1	353586	3360.6	4009.7	2726.9	4552.3	4534.9	3179.5
DQ334667.1	199082	7879.7	7102.7	3117.2	6960.5	9431.5	7587.3
DQ334608.1	188421	5386.7	5807.9	6246.5	4221.9	6303.7	7100.1
EF125390.1	195498	7026.4	7279.4	10813.7	6410.3	12802.0	12586.8
EU617839.1	307096	14125.4	13621.8	11912.8	10647.2	18722.2	12778.9
AY225608.1	98504	5253.8	5252.1	3438.6	6808.8	9919.3	6976.7
EF126277.1	259881	1498.6	2648.6	6944.0	1570.6	2795.6	2834.6
AM936555.1	554552	1496.1	2266.5	3502.5	2082.2	2541.8	2881.6
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GQ111138.1	380727	1338.7	1985.6	3458.4	837.3	1829.0	1366.2
EU134492.1	244127	256.1	411.6	1423.1	175.9	245.1	1122.0
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AY922176.1	114327	11593.5	10990.1	9873.1	8368.6	7029.5	9213.6
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GQ024961.1 gg_id:484709 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1:
EU617830.1 gg_id:327954 Seasonal variation microbial Yel Sea sediment clone C13S-5
FJ748770.1 gg_id:588676 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar
EU386047.1 gg_id:275298 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
FJ484789.1 gg_id:545469 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
EF516387.1 gg_id:219204 grassland soil clone FCPS600
EU134554.1 gg_id:254386 tallgrass prarie soil clone FFCH3001
DQ067034.1 gg_id:136119 Lake Washington sediment clone pLW-43
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EF646124.1 gg_id:251921 Potential interactions particle- anammox and archaeal partners namibian Namibian u
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DQ331000.1 gg_id:159288 Guerrero Negro hypersaline microbial mat clone 09D2Z35
DQ017950.1 gg_id:131476 upland stream clone S-Btb7_59
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EU134552.1	254949	9377.9	9802.8	13165.3	8598.9	12156.6	11750.3
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EU617830.1	327954	1034.1	2501.8	757.2	523.7	2190.3	2629.1
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EU386047.1	275298	2993.9	2923.8	6591.6	3629.7	3253.6	3461.9
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EF516387.1	219204	5189.3	5898.8	5805.9	6620.3	6337.6	6327.3
EU134554.1	254386	3917.4	5137.4	7342.5	5048.7	7103.8	6658.6
DQ067034.1	136119	3291.0	4611.0	5811.2	2657.0	3954.9	4041.5
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DQ109897.1	144289	1028.9	1878.9	4709.3	2393.6	1123.8	2771.1
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EF646143.1	236868	4868.4	5187.8	7182.9	2900.0	7953.5	6533.3
DQ269115.1	198233	227.5	338.1	766.3	229.1	246.4	240.7
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FJ416092.1 gg_id:361919 sediments sediment station NEC5 Northern Bering Sea clone 047M27
AY869685.1 gg_id:112279 ridge flank crustal fluids clone FS266-77B-03
EU919813.1 gg_id:351152 Kongsfjorden western Spitsbergen Svalbard ocean water clone b132
DQ015820.1 gg_id:140293 Antarctic lake water clone ELB19-125
DQ396146.1 gg_id:154831 deep-sea octacoral clone ctg_NISA283
DQ289938.1 gg_id:162701 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
FJ203381.1 gg_id:333342 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AY869686.1 gg_id:111722 ridge flank crustal fluids clone FS266-91B-03
FM179869.1 gg_id:354477 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl
DQ396052.1 gg_id:203027 deep-sea octacoral clone ctg_NISA259
EU925877.1 gg_id:355585 sediments sediment station DBS1 northern Bering Sea clone 082F74
EU491634.1 gg_id:268705 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AM997336.1 gg_id:559828 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU491229.1 gg_id:262635 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ070808.1 gg_id:145961 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
FM201096.1 gg_id:565517 and distinct induced biofilm fouling operated under conditions laboratory-scale men
AB278147.1 gg_id:178175 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar
AB015243.1 gg_id:10680 deepest cold-seep area Japan Trench clone JTB38 proteobacterium
EU491278.1 gg_id:264210 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ070816.1 gg_id:148800 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
EU734958.1 gg_id:328791 assemblages sediment station DBSE Northern Bering Sea clone 051C67
AM936257.1 gg_id:557373 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AF317744.1 gg_id:136925 Nullarbor cave clone wb1_A15
EU287161.1 gg_id:235691 Pacific arctic surface sediment clone P13-68
AB252955.1 gg_id:170623 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 127
FM253643.1 gg_id:334324 Rock gold mine unusually microbial biofilm clone C01-2
EU048674.1 gg_id:250443 and archaeal surface marine sediment Slope South China Sea clone MD2896-B15
FJ416121.1 gg_id:357893 sediments sediment station NEC5 Northern Bering Sea clone 107N50
AM997837.1 gg_id:556644 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU287148.1 gg_id:236118 Pacific arctic surface sediment clone P13-55
AM997677.1 gg_id:573417 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU734949.1 gg_id:309636 assemblages sediment station DBSE Northern Bering Sea clone 041C44
GQ261757.1 gg_id:554666 shifts taxa and response localized organic loading deep sea sediment whale falls clo
EU734974.1 gg_id:325961 assemblages sediment station DBSE Northern Bering Sea clone 068C78
EU287128.1 gg_id:250580 Pacific arctic surface sediment clone P13-35
EU290680.1 gg_id:253113 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
EF208656.1 gg_id:200746 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2
EU734976.1 gg_id:325676 assemblages sediment station DBSE Northern Bering Sea clone 070C81

AJ534630.1	75196	391.4	770.5	3144.2	200.7	174.5	185.2
DQ129243.1	137768	229.2	682.3	2666.1	203.8	4596.4	3793.4
AF421890.1	70239	178.3	383.2	2459.6	303.2	1359.4	712.0
FJ416092.1	361919	1822.1	2345.8	2216.2	1527.0	3509.5	2883.2
AY869685.1	112279	47.1	107.9	85.3	74.0	56.4	27.7
EU919813.1	351152	7068.8	6618.0	7085.5	7348.8	6286.2	8486.4
DQ015820.1	140293	4212.7	5143.8	5304.4	7965.5	5247.3	4980.9
DQ396146.1	154831	7497.3	9516.7	8246.4	9325.5	11244.8	11075.1
DQ289938.1	162701	4587.3	5248.1	8426.8	4260.8	4280.9	5335.0
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DQ396052.1	203027	10307.9	11835.7	9629.3	10902.3	11304.5	8837.2
EU925877.1	355585	6267.4	8188.9	4088.2	6479.2	6243.0	4731.9
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AM997336.1	559828	6871.5	6921.4	9534.3	9630.2	5982.4	8763.4
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DQ070808.1	145961	4303.1	5341.5	4822.9	4182.5	7852.4	6295.9
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FJ416121.1	357893	5326.1	6049.8	6671.8	4441.0	5519.8	4494.4
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EU287148.1	236118	2713.7	2566.2	1543.3	1641.8	4870.7	3719.8
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EU734974.1	325961	1080.6	1358.4	2017.2	1101.6	604.2	447.0
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EU734976.1	325676	10023.6	11795.7	6523.8	10703.4	14655.1	15900.7

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EU925834.1 gg_id:315157 sediments sediment station DBS1 northern Bering Sea clone 001E3
FJ479395.1 gg_id:591473 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ289896.1 gg_id:165188 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
EU050853.1 gg_id:246832 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_08_44
EU373896.1 gg_id:263721 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
FJ203391.1 gg_id:349173 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
FJ416109.1 gg_id:359523 sediments sediment station NEC5 Northern Bering Sea clone 084L59
GQ246453.1 gg_id:562069 Temporal and spatial China North Yel Sea sediments clone Ld1-58
FM179874.1 gg_id:327682 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl
EU652604.1 gg_id:278639 Seasonal variation microbial Yel Sea sediment clone B8S-84
FJ358879.1 gg_id:563535 and redox-stratified sediments marine reef sandy sediment clone OX62
DQ676409.1 gg_id:223862 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AM935311.1 gg_id:564760 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ129097.2 gg_id:195967 forest soil clone CWT SM02_H11
EU234198.1 gg_id:236923 receiving river and un techniques effluent WWTP treating penicillin G production wa
AB252953.1 gg_id:165369 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 024
EU617842.1 gg_id:348822 Seasonal variation microbial Yel Sea sediment clone D13S-27
GU118825.1 gg_id:542878 Threatened Corals Provide Microbial Habitats clone Mfra_O14
DQ395065.1 gg_id:150819 harbor sediment clone VHS-B5-73
AF354155.1 gg_id:71658 marine methane seep clone 1510
EU734963.1 gg_id:344456 assemblages sediment station DBSE Northern Bering Sea clone 057D15
EU236344.1 gg_id:296500 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2H11
AF317771.1 gg_id:136770 Nullarbor cave clone wb1_N15
GU230398.1 gg_id:581179 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo
FJ358881.1 gg_id:588965 and redox-stratified sediments marine reef sandy sediment clone SO51
EU287101.1 gg_id:255323 Pacific arctic surface sediment clone P13-8
EU050852.1 gg_id:236169 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_01_50
AM935597.1 gg_id:561217 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ787717.1 gg_id:163996 holocene lake sediment clone SLB622
AM936057.1 gg_id:542911 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AF154103.1 gg_id:10724 hydrocarbon seep clone GCA047
DQ331004.1 gg_id:159301 Guerrero Negro hypersaline microbial mat clone 10D2Z33
AM490745.1 gg_id:592584 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
GU362952.1 gg_id:555750 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
AF154094.1 gg_id:10677 hydrocarbon seep clone BPC065
EU246004.1 gg_id:253746 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-D07
EU360307.1 gg_id:277150 microbial fuel cell enriched sediment clone FWS 711
DQ109919.1 gg_id:143327 Sulfate-reducing mats: Changing paradigms new discoveries salt pond nonlithifying
DQ676442.1 gg_id:217352 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
CP001322.1 gg_id:514785 Desulfatibacillum alkenivorans str. AK-01
AY493562.1 gg_id:103090 Desulfatibacillum alkenivorans str. PF2803

EU925834.1	315157	3408.6	3353.8	5625.7	3291.8	2773.8	4989.1
FJ479395.1	591473	49.8	107.3	120.7	74.3	248.5	237.7
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EU050853.1	246832	3007.6	2258.6	1691.2	3966.9	4876.4	4486.1
EU373896.1	263721	6751.3	5622.5	5491.3	5798.4	4635.8	5586.1
FJ203391.1	349173	1787.5	2571.5	3704.0	2391.5	6974.7	5937.8
FJ416109.1	359523	6362.9	7114.3	9141.3	5801.0	8630.0	6944.2
GQ246453.1	562069	5090.7	5835.1	9293.1	4620.9	8431.2	7197.3
FM179874.1	327682	9969.8	14069.8	11041.6	10372.1	15932.9	14031.6
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FJ358879.1	563535	4134.5	4522.9	6920.9	5181.1	7606.5	7956.0
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EU050852.1	236169	3497.0	2768.6	4629.1	3561.2	7917.2	4789.8
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DQ787717.1	163996	668.1	1319.2	2685.0	1200.3	439.4	1495.5
AM936057.1	542911	1173.7	2506.4	8301.1	1792.5	2680.4	2666.5
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EU360307.1	277150	4388.4	5438.8	8646.3	6856.9	4938.8	5861.4
DQ109919.1	143327	31.9	96.2	234.3	71.9	60.6	37.5
DQ676442.1	217352	46.1	121.6	354.0	66.2	124.9	58.0
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AY184360.2 gg_id:79514 Desulfatibacillum aliphaticivorans str. CV2803
AF418175.1 gg_id:74171 Desulfobacter curvatus str. DSM 3379
NR_025348.1 gg_id:572343 Desulfobacterium anilini str. Ani1; DSM 4660
CP001087.1 gg_id:523103 Desulfobacterium autotrophicum str. HRM2
AY542197.1 gg_id:113166 Gulf Mexico seafloor sediments clone GoM HDB-06
AF026998.1 gg_id:10771 hot spring clone OPB16
AY771951.1 gg_id:111847 marine surface sediment clone SI28
GU362956.1 gg_id:533418 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
EU385666.1 gg_id:262547 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
AF029045.1 gg_id:10904 Benzene mineralizing consortium complete clone SB-21 consortium
FJ716478.1 gg_id:566769 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water
FJ485020.1 gg_id:566534 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114
GQ356929.1 gg_id:544180 Metal Dependent Marine Methane Oxidation methane seep sediment clone Fe_B_1
AF029048.1 gg_id:10906 Benzene mineralizing consortium complete clone SB-30 consortium
DQ330997.1 gg_id:159166 Guerrero Negro hypersaline microbial mat clone 09D2Z19
AY592183.1 gg_id:99181 marine ANAMMOX sediment clone AY592183
FJ628304.1 gg_id:564870 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
FN396628.1 gg_id:565202 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_II
FJ437822.1 gg_id:535056 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa
DQ109878.1 gg_id:142790 Sulfate-reducing mats: Changing paradigms new discoveries salt pan lithifying micro
AB177158.1 gg_id:132816 seafloor methane hydrate clone ODP1230B17.18
GU180164.1 gg_id:540242 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
AM086120.1 gg_id:145576 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
AM745206.1 gg_id:294510 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
EU385798.1 gg_id:274378 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU385717.1 gg_id:276920 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU925857.1 gg_id:328502 sediments sediment station DBS1 northern Bering Sea clone 052E88
FM164951.2 gg_id:395222 two Bulgarian geothermal springs hot spring clone S1-53
DQ811822.1 gg_id:164969 mangrove soil clone MSB-5A4
EU245381.1 gg_id:238545 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-A0
AY542227.1 gg_id:113116 Gulf Mexico seafloor sediments clone GoM IDB-15
AM229200.1 gg_id:575796 Microbial vicinity and within hydrates Hydrate Ridge (Cascadia Margin) marine gas
EU385917.1 gg_id:270552 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
GU302479.1 gg_id:557390 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat
EU592476.1 gg_id:592826 Seasonal changes Salton Sea hypersaline sediment clone SSS17A
DQ521799.1 gg_id:159904 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexico
FN429786.1 gg_id:548583 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
FJ264650.1 gg_id:339335 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
DQ676438.1 gg_id:221104 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
DQ925877.1 gg_id:252087 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
AB015244.1 gg_id:10939 deepest cold-seep area Japan Trench clone JTB133 proteobacterium

AY184360.2	79514	2749.2	2975.2	3885.5	1874.1	3414.5	4797.5
AF418175.1	74171	64.9	89.3	622.9	265.0	73.5	29.5
NR_025348.1	572343	24.5	31.9	14.8	50.8	52.9	12.1
CP001087.1	523103	2069.2	2613.1	5523.5	3061.7	4679.8	4143.5
AY542197.1	113166	1511.1	1976.4	3955.0	1039.5	2083.4	1701.3
AF026998.1	10771	192.2	395.5	351.0	401.0	356.9	418.3
AY771951.1	111847	113.1	118.2	270.7	166.9	149.1	74.3
GU362956.1	533418	769.5	1502.1	1008.4	565.4	311.5	617.0
EU385666.1	262547	10130.1	11123.4	12741.5	6677.4	10332.0	10207.1
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FJ716478.1	566769	1139.7	2407.3	5658.9	1036.2	1522.0	1665.6
FJ485020.1	566534	7177.7	8544.7	11951.1	10158.3	9244.3	10728.7
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AY592183.1	99181	22.0	57.5	33.3	37.2	70.2	16.6
FJ628304.1	564870	6388.1	7574.7	7299.9	6097.8	9308.3	7279.4
FN396628.1	565202	1467.1	1555.9	2350.1	2729.1	1812.7	2109.7
FJ437822.1	535056	5377.0	5462.9	4126.0	6106.0	9283.8	7108.3
DQ109878.1	142790	23.4	53.7	18.3	48.3	56.2	20.4
AB177158.1	132816	10984.0	12702.0	4617.7	7597.7	9618.3	8325.1
GU180164.1	540242	3287.4	2989.8	4168.3	1101.0	1288.4	1418.2
AM086120.1	145576	25.3	33.6	21.2	52.6	74.7	26.9
AM745206.1	294510	461.3	938.5	1084.7	255.2	669.9	1740.7
EU385798.1	274378	2714.9	2803.7	5449.5	4046.1	1123.4	2389.7
EU385717.1	276920	98.4	170.2	156.5	123.4	153.1	122.9
EU925857.1	328502	94.3	188.4	177.5	92.0	59.1	65.6
FM164951.2	395222	5492.1	6951.1	8316.7	5455.5	6338.1	7524.6
DQ811822.1	164969	37.2	144.1	139.6	68.8	77.7	40.7
EU245381.1	238545	3741.9	4504.3	5097.8	4227.0	4565.1	4254.3
AY542227.1	113116	23.7	33.3	29.3	59.8	74.5	23.0
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DQ521799.1	159904	4914.6	5916.7	8118.0	4872.9	3060.3	4325.5
FN429786.1	548583	2018.0	2859.5	4718.1	2102.2	2922.1	3109.6
FJ264650.1	339335	170.3	336.7	318.2	116.5	84.1	74.4
DQ676438.1	221104	3875.3	2413.2	3197.4	3803.2	420.2	3541.7
DQ925877.1	252087	3717.8	3718.0	6663.8	4572.1	10103.2	5013.9
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U85471.1 gg_id:10941 Desulfobacterium sp. str. BG18
AY197382.1 gg_id:86333 Guaymas Basin hydrothermal vent sediments clone B01R011
AY197376.1 gg_id:86388 Guaymas Basin hydrothermal vent sediments clone B01R004
AJ441316.1 gg_id:67542 Desulfobacula toluolica str. DSM 7467
CP000859.1 gg_id:255870 Desulfococcus oleovorans str. Hxd3
DQ103668.1 gg_id:132520 hypersaline endoevaporitic microbial mat clone E4aE11
GQ249552.1 gg_id:546119 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
EU246073.1 gg_id:238062 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-H01
DQ397423.1 gg_id:159502 Guerrero Negro hypersaline microbial mat clone 04D2Z68
GQ249596.1 gg_id:544699 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
FJ712553.1 gg_id:521361 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AM176871.1 gg_id:160902 Recovery mangrove sediment clone SZB46
EU245312.1 gg_id:257695 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-H01
EU245273.1 gg_id:256695 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B05
AF513951.1 gg_id:111956 hypersaline lake clone LA30-B27
AJ620510.1 gg_id:108098 Olavius crassitunicatus endosymbiont
EU245134.1 gg_id:241850 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-G0
AF099063.1 gg_id:10900 Desulfofaba gelida str. PSv29
AB015240.1 gg_id:10907 deepest cold-seep area Japan Trench clone JTB16
NR_028732.1 gg_id:592871 Desulfofrigus fragile str. LSv21; DSM 12345
AB189366.1 gg_id:113570 cold seep sediment clone JT75-121
FM242377.1 gg_id:349097 sequences sediment clone 19 T9d+oil
EF125385.1 gg_id:194587 soil naked tidal flat sediment near mangrove clone MSB-1ax8
FM242229.1 gg_id:322751 sequences sediment clone 96 T0h-oil
AB530178.1 gg_id:583955 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba
DQ351771.1 gg_id:147847 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
EF442994.1 gg_id:248725 Desulfotignum sp. str. DSM 7120
AF233370.1 gg_id:31826 Desulfotignum balticum str. Sax (DSM 7044) marine mud
EU047532.1 gg_id:251611 Anaerobic degradation benzene marine and cell hybridization dominant phylotype b
EU047529.1 gg_id:235729 Anaerobic degradation benzene marine and cell hybridization dominant phylotype b
AM882605.1 gg_id:330092 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU386050.1 gg_id:264473 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AB240476.1 gg_id:143077 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
EU048686.1 gg_id:245974 and archaeal surface marine sediment Slope South China Sea clone MD2896-B29
EF454380.2 gg_id:222931 termite hindgut clone 290cost002-P3L-2033
EU487868.1 gg_id:561085 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU885093.1 gg_id:305714 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2A5
FJ712462.1 gg_id:526057 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EF454653.2 gg_id:226987 termite hindgut clone 290cost002-P3L-2488
EU622291.1 gg_id:289758 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Ri
AM490751.1 gg_id:537744 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir

U85471.1	10941	39.9	76.5	123.3	116.1	69.5	138.1
AY197382.1	86333	58.1	107.5	166.1	96.4	73.7	40.6
AY197376.1	86388	85.2	192.5	75.7	72.0	89.6	43.5
AJ441316.1	67542	534.1	801.1	796.6	997.1	172.7	554.0
CP000859.1	255870	50.4	99.0	137.6	74.2	67.5	33.4
DQ103668.1	132520	912.3	2263.0	5321.0	1247.7	4068.4	5566.8
GQ249552.1	546119	696.6	2783.1	4511.2	703.9	204.9	404.3
EU246073.1	238062	6439.1	9776.4	9386.3	7252.4	8641.3	11437.0
DQ397423.1	159502	3590.0	4078.6	5031.6	3733.3	6475.4	6608.8
GQ249596.1	544699	549.3	2003.8	3792.1	500.1	164.1	602.7
FJ712553.1	521361	2700.6	3364.9	2438.7	3785.4	3957.4	3036.9
AM176871.1	160902	971.4	2960.0	3435.7	915.2	1133.1	883.9
EU245312.1	257695	1641.5	1207.3	360.7	336.4	478.7	84.7
EU245273.1	256695	2526.0	2107.4	2828.1	1832.8	2298.7	2752.4
AF513951.1	111956	44.9	115.2	353.1	99.3	71.8	80.1
AJ620510.1	108098	84.7	293.3	363.9	118.7	368.4	76.8
EU245134.1	241850	6452.4	8129.4	11564.4	9366.8	10925.2	11199.3
AF099063.1	10900	2495.7	3201.0	5669.7	2029.4	2788.6	2410.1
AB015240.1	10907	800.4	1326.0	960.3	1622.5	3954.4	2554.9
NR_028732.1	592871	1786.0	1405.9	3185.1	1583.9	798.7	1140.7
AB189366.1	113570	1668.2	2515.0	3141.9	2143.8	3547.6	2915.9
FM242377.1	349097	2629.1	3603.2	5010.6	2324.6	6507.8	4438.6
EF125385.1	194587	4958.4	5010.4	3762.0	5029.8	3050.5	3953.5
FM242229.1	322751	1816.5	1814.8	1227.4	315.3	114.7	179.6
AB530178.1	583955	3047.8	3160.9	1766.1	3624.7	5314.1	3734.3
DQ351771.1	147847	10675.6	10486.3	2911.3	7859.0	10492.7	8734.4
EF442994.1	248725	6188.8	5984.8	4740.0	5359.0	9604.9	7316.1
AF233370.1	31826	7862.2	7237.5	5249.6	6577.6	6163.0	7395.3
EU047532.1	251611	2224.3	3848.5	1440.5	3421.0	562.8	715.4
EU047529.1	235729	1090.8	1166.9	2638.7	791.6	1589.7	991.0
AM882605.1	330092	4450.8	5348.0	2148.2	5268.2	8323.8	6330.3
EU386050.1	264473	6200.6	6331.0	4421.3	5013.2	7106.0	6575.6
AB240476.1	143077	1585.6	2385.6	1604.8	1214.1	2842.2	1563.6
EU048686.1	245974	3542.5	4204.2	6087.4	4398.4	6484.4	5113.0
EF454380.2	222931	14060.5	14607.9	13146.8	11439.4	14564.1	13612.2
EU487868.1	561085	2972.5	5296.4	6423.3	1732.8	2808.4	3034.3
EU885093.1	305714	5113.8	6670.4	6596.3	4299.4	3632.9	4635.6
FJ712462.1	526057	2428.6	2962.9	2549.1	2189.6	6991.7	4904.4
EF454653.2	226987	4690.6	6267.2	3666.0	3236.0	6962.3	6256.6
EU622291.1	289758	2632.0	2584.0	1914.5	3327.9	6144.1	5795.4
AM490751.1	537744	5097.9	4407.6	3511.6	3450.3	3784.8	4415.3

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GQ844347.1 gg_id:542030 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-HE
EF454687.2 gg_id:223294 termite hindgut clone 290cost002-P3L-2541
AY542569.1 gg_id:113399 Gulf Mexico seafloor sediment clone GoM GB425 12B-61
FJ484450.1 gg_id:571089 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AB234533.1 gg_id:145609 termite gut homogenate clone MgMjD-089
AB240382.1 gg_id:150612 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
EU246159.1 gg_id:248560 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E05
FJ516879.1 gg_id:552734 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
AM882604.1 gg_id:333017 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU385937.1 gg_id:262118 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
AM882591.1 gg_id:327370 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
DQ831539.1 gg_id:171382 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
EU246034.1 gg_id:249930 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-H08
AM086154.1 gg_id:147459 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
EF014726.1 gg_id:225865 Candidatus Magnetoglobus multicelularis gen. sp. nov. multicellular magnetotactic p
AM086124.1 gg_id:146208 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
EF442981.1 gg_id:237295 Desulfocella sp. str. DSM 2056
EU399670.1 gg_id:273059 and localization microbial consortium full-scale granular activated carbon anaerobic
FJ264667.1 gg_id:311003 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AY222309.1 gg_id:113207 host hindgut caecum clone Del 19
DQ811835.1 gg_id:173313 mangrove soil clone MSB-5E7
U45989.1 gg_id:10869 Desulfonema magnum str. DSM 2077 anaerobic mud seawater lagoon (Etang de Prevost
AB189380.1 gg_id:114027 cold seep sediment clone JT75-319
AB188779.1 gg_id:113838 cold seep sediment clone SB3-7
FJ789839.1 gg_id:534671 Desulfobotulus sapovorans str. ATCC 33892; 1pa3
FM242270.1 gg_id:314257 sequences sediment clone 4 T0h-oil
EU160523.1 gg_id:352459 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
FJ202141.1 gg_id:314793 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU385675.1 gg_id:272166 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
DQ395063.1 gg_id:156126 harbor sediment clone VHS-B5-66
DQ397412.1 gg_id:159381 Guerrero Negro hypersaline microbial mat clone 02D2Z96
DQ811836.1 gg_id:173385 mangrove soil clone MSB-5F12
AJ937698.1 gg_id:143680 Microbiological investigation methane- and hydrocarbon-discharging volcanoes Carp
AY222304.1 gg_id:114278 host hindgut caecum clone Del 1
AM882599.1 gg_id:326082 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
AB355082.1 gg_id:237712 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma
EU622295.1 gg_id:294941 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv
FJ716993.1 gg_id:544106 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
DQ630689.1 gg_id:159784 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp5
EU570889.1 gg_id:556574 transition and zone within near-shore anoxic basin: Nitinat Lake depth 50 m clone Ni
U85470.1 gg_id:10934 Desulfobotulus sp. str. BG14

GQ844347.1	542030	537.4	1877.2	4640.4	465.8	375.6	940.9
EF454687.2	223294	8757.5	9317.7	6480.4	7593.3	7551.4	6751.8
AY542569.1	113399	579.8	592.9	939.0	502.8	1122.9	1021.8
FJ484450.1	571089	3401.6	4111.8	6680.7	4169.0	4259.3	6041.4
AB234533.1	145609	4186.9	4345.4	3398.2	3800.5	2968.4	3262.7
AB240382.1	150612	1347.3	1246.8	2232.3	846.4	2443.8	2868.9
EU246159.1	248560	145.2	242.0	642.1	97.6	122.1	125.8
FJ516879.1	552734	269.0	871.0	2550.8	256.5	671.5	325.6
AM882604.1	333017	8423.9	11670.4	11834.2	9185.0	13557.4	15429.6
EU385937.1	262118	4657.1	4538.3	5493.2	6922.8	2613.3	3147.3
AM882591.1	327370	5349.6	5247.6	2049.9	6491.8	6975.4	6000.9
DQ831539.1	171382	3387.3	3961.9	4822.9	2520.2	3430.2	2877.8
EU246034.1	249930	1699.8	1859.5	1843.2	1313.5	349.4	1147.1
AM086154.1	147459	343.9	973.8	1328.7	155.8	265.1	284.7
EF014726.1	225865	4299.1	4834.6	8861.4	5279.3	6072.2	6712.7
AM086124.1	146208	30.3	42.6	45.0	67.3	77.5	39.0
EF442981.1	237295	48.8	131.3	210.6	37.8	199.7	138.1
EU399670.1	273059	920.3	3995.2	700.8	163.8	1115.3	307.7
FJ264667.1	311003	16.1	93.0	568.0	102.1	145.0	57.8
AY222309.1	113207	20.1	24.0	18.9	47.9	56.3	17.0
DQ811835.1	173313	405.0	366.2	269.0	273.5	532.4	530.6
U45989.1	10869	50.1	162.0	58.0	80.4	58.9	31.9
AB189380.1	114027	293.1	433.5	2310.8	556.6	96.1	91.0
AB188779.1	113838	2632.2	2477.3	1270.0	1261.9	1386.4	1769.1
FJ789839.1	534671	462.3	573.3	1048.8	217.9	330.0	764.3
FM242270.1	314257	1702.3	1616.3	1746.8	1234.2	337.6	574.6
EU160523.1	352459	1770.1	3664.2	6533.3	2369.6	5455.7	6350.6
FJ202141.1	314793	46.9	92.9	166.4	70.9	79.7	58.9
EU385675.1	272166	5721.4	5931.2	6698.6	4675.0	5412.7	4844.1
DQ395063.1	156126	74.8	261.3	127.9	154.7	363.6	226.3
DQ397412.1	159381	3776.8	2049.0	3254.2	5048.8	1902.5	3085.1
DQ811836.1	173385	909.2	678.8	1032.8	433.9	352.2	323.1
AJ937698.1	143680	9874.7	10268.0	5637.2	8021.4	1532.7	843.4
AY222304.1	114278	4681.9	3837.0	2873.5	6456.7	3079.9	3172.5
AM882599.1	326082	1457.0	926.2	1622.8	1112.6	226.6	939.3
AB355082.1	237712	17097.1	18324.2	9124.6	13921.1	16299.1	13639.2
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FJ716993.1	544106	101.8	141.4	198.9	138.2	272.9	76.8
DQ630689.1	159784	8603.3	8989.1	6211.6	3957.7	3343.7	2762.1
EU570889.1	556574	342.5	1176.3	4460.1	556.2	832.6	1195.7
U85470.1	10934	1294.3	2593.8	2184.7	600.4	2549.5	2546.1

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FJ264753.1 gg_id:313386 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
DQ397424.1 gg_id:159185 Guerrero Negro hypersaline microbial mat clone 04D2Z24
AM882642.1 gg_id:320845 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU592487.1 gg_id:563232 Seasonal changes Salton Sea hypersaline sediment clone SSS3A
FJ712404.1 gg_id:520767 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
NR_025406.1 gg_id:544630 Desulfococcus biacutus str. DSM 5651
DQ831540.1 gg_id:165612 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
AB294926.1 gg_id:225575 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
EU290724.1 gg_id:253758 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
FM242446.1 gg_id:341474 sequences sediment clone 50 T12d+oil
EU386062.1 gg_id:275331 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
FM165241.1 gg_id:557184 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone
FJ973581.1 gg_id:378495 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu
FJ712482.1 gg_id:528626 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
FJ485367.1 gg_id:566855 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AY082457.1 gg_id:67851 neutral pH mine biofilm clone 44a-B1-10
DQ630675.1 gg_id:160459 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp23
EF125398.1 gg_id:189923 soil naked tidal flat sediment near mangrove clone MSB-1cx7
AJ704678.1 gg_id:109279 marine sediment clone HMMVPog-2
DQ415842.1 gg_id:157733 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
FN396636.1 gg_id:541666 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_II
GU230401.1 gg_id:554116 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo
AY216443.1 gg_id:81354 temperate estuarine mud clone KM88
DQ630707.1 gg_id:160788 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp2_2
DQ521813.1 gg_id:160182 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic
FM242231.1 gg_id:317203 sequences sediment clone 189 T0h-oil
FJ716967.1 gg_id:545744 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
AJ704696.1 gg_id:109295 marine sediment clone HMMVBeg-44
GQ356986.1 gg_id:581992 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_
GQ249585.1 gg_id:587834 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer c
AM882600.1 gg_id:306625 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
FJ814756.1 gg_id:556875 Microbial assemblages Thioploca sheaths cold seep settings Monterey Bay Carmel Ca
EU487979.1 gg_id:574128 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
AJ237607.1 gg_id:10870 Desulfobacterium indolicum str. DSM 3383 marine mud
AY771939.1 gg_id:111869 marine surface sediment clone SI29
EU385785.1 gg_id:272732 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
GQ433957.1 gg_id:590151 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst
AY592200.1 gg_id:99952 marine ANAMMOX sediment clone AY592200
FJ517109.1 gg_id:549171 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
EU385687.1 gg_id:274595 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
AM882587.1 gg_id:340294 Structure along hydrocarbon contamination coastal sediment oil polluted water pet

FJ264753.1	313386	1726.6	2664.5	4491.1	3143.1	6224.6	5063.1
DQ397424.1	159185	434.1	323.7	685.9	283.9	434.5	380.5
AM882642.1	320845	1057.5	2688.3	4331.1	1683.3	1518.1	1909.2
EU592487.1	563232	2693.0	5528.0	3876.8	1829.4	5748.9	4578.7
FJ712404.1	520767	5528.4	4552.3	4000.9	7153.7	8856.9	7210.5
NR_025406.1	544630	345.8	1192.1	2049.1	336.8	347.5	511.1
DQ831540.1	165612	1958.6	2052.5	4965.4	2834.8	2212.2	2318.2
AB294926.1	225575	678.8	1316.5	2832.7	1018.3	2239.9	2864.7
EU290724.1	253758	11189.5	12690.3	13156.4	9711.3	11526.5	11603.8
FM242446.1	341474	138.4	213.2	345.1	100.0	75.1	132.8
EU386062.1	275331	4876.2	5195.7	8803.1	4138.3	2539.0	4537.7
FM165241.1	557184	3409.2	4007.1	5414.9	3848.3	4273.5	4431.5
FJ973581.1	378495	3465.9	4031.6	10080.3	4634.4	6009.1	4419.5
FJ712482.1	528626	6603.7	6618.1	3392.4	7441.9	7516.9	6102.0
FJ485367.1	566855	5933.0	8123.0	9373.2	6310.7	5858.9	4432.1
AY082457.1	67851	38.9	112.9	79.3	80.9	73.9	31.6
DQ630675.1	160459	9934.9	11024.0	12350.8	8596.5	11436.0	10404.5
EF125398.1	189923	92.9	151.0	111.5	85.9	150.8	55.4
AJ704678.1	109279	29.6	74.4	59.6	60.6	59.8	44.6
DQ415842.1	157733	69.9	108.9	135.0	100.7	57.7	37.1
FN396636.1	541666	71.0	179.3	296.1	46.4	48.8	20.1
GU230401.1	554116	1780.9	2176.7	3087.4	1961.3	1581.2	2537.6
AY216443.1	81354	1618.3	2580.2	1080.6	2141.1	2422.4	2627.1
DQ630707.1	160788	229.8	667.3	735.6	141.5	57.1	83.5
DQ521813.1	160182	60.1	245.9	82.9	47.0	42.9	38.6
FM242231.1	317203	3766.0	3673.1	1425.8	4593.7	7008.1	6104.0
FJ716967.1	545744	5977.1	7419.2	5344.8	8754.3	5366.6	5266.9
AJ704696.1	109295	7698.2	9454.7	9421.0	7488.4	6940.0	5989.4
GQ356986.1	581992	2078.2	2777.4	1861.9	3764.2	2280.9	2510.6
GQ249585.1	587834	41.9	117.2	222.9	72.5	336.5	45.0
AM882600.1	306625	1421.5	1767.3	1210.6	958.1	82.0	307.4
FJ814756.1	556875	1786.0	3404.9	2945.8	1634.1	1708.4	1641.8
EU487979.1	574128	3841.1	5680.8	9247.5	3464.6	6255.3	5894.2
AJ237607.1	10870	33.6	75.1	72.2	63.8	80.9	90.8
AY771939.1	111869	41.0	183.4	755.4	84.7	500.5	577.0
EU385785.1	272732	1648.3	3277.8	5677.8	1771.4	2592.7	2697.6
GQ433957.1	590151	2199.0	2406.5	4864.9	2404.6	1267.3	2822.1
AY592200.1	99952	39.9	97.3	21.9	46.2	55.1	19.6
FJ517109.1	549171	701.9	980.2	871.1	1376.8	229.4	496.1
EU385687.1	274595	2994.0	4185.2	10305.1	2899.7	3157.1	3877.4
AM882587.1	340294	719.9	1293.2	574.2	430.2	1646.3	2095.7

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DQ330998.1 gg_id:159453 Guerrero Negro hypersaline microbial mat clone 09D2Z88
EF125423.1 gg_id:184819 mangrove soil clone MSB-2A5
AY053490.1 gg_id:39986 gas hydrate clone AT425_EubD9
AJ620501.1 gg_id:353759 Olavius 3 endosymbiont O. ilvae Individual 5
FJ746111.1 gg_id:513493 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
DQ811817.1 gg_id:172929 mangrove soil clone MSB-4G8
FM242225.1 gg_id:337177 sequences sediment clone 342 T0h-oil
AB237684.1 gg_id:139771 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW
AY082461.1 gg_id:67845 neutral pH mine biofilm clone 44a-B1-17
GU302442.1 gg_id:552223 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat
AM774314.1 gg_id:243934 Cultivation and situ quantification consistently demonstrate that two distinct group
EF999398.1 gg_id:237632 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn
DQ630706.1 gg_id:161002 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp2_28
AJ241022.1 gg_id:10909 Norway:(Svalbard)Hornsund clone Sva0405
DQ831553.1 gg_id:163459 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
AJ831748.1 gg_id:102310 chemocline clone 166
DQ146482.1 gg_id:164141 Desulfobacterium sp. MB-2005
DQ630702.1 gg_id:160395 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp2_20
FJ716406.1 gg_id:571102 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water
AY851291.1 gg_id:148326 Algidimarina propionica str. AK-P
EF688206.1 gg_id:347101 Detection microbial sludge anaerobic wastewater treatment system clone 5A4_cons
EU717681.1 gg_id:425208 Ultrastructure tactic behaviour and potential sulfate reduction multicellular magnetc
U81720.2 gg_id:10893 anaerobic digestor clone vadinHA60
GQ356954.1 gg_id:576546 Metal Dependent Marine Methane Oxidation methane seep sediment clone Fe_B_1
DQ811793.1 gg_id:173340 mangrove soil clone MSB-3ax11
AB177130.1 gg_id:130033 seafloor methane hydrate clone ODP1230B1.06
AM774320.1 gg_id:248513 Cultivation and situ quantification consistently demonstrate that two distinct group
EU160501.1 gg_id:325508 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
U45991.1 gg_id:10897 Desulfonema ishimotonii str. DSM 9679 anaerobic intertidal mud flats Jadebusen (North
EU617853.1 gg_id:345458 Seasonal variation microbial Yel Sea sediment clone D13S-20
EU246163.1 gg_id:248972 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E10
AM404371.1 gg_id:558344 Hydrocarbon-fueled sulfate reduction can sustain long-lived tubeworm aggregation
AJ620497.1 gg_id:354146 Olavius 4 endosymbiont O. algarvensis Individual 2
DQ811815.1 gg_id:167112 mangrove soil clone MSB-4G4
DQ811807.1 gg_id:166757 mangrove soil clone MSB-4C12
DQ397413.1 gg_id:159387 Guerrero Negro hypersaline microbial mat clone 02D2Z34
AJ831753.1 gg_id:106553 chemocline clone 293
DQ004679.1 gg_id:158084 Microbial Reduce Methane Efflux Mud Volcano Sediments Gulf Cadiz marine hydroc
U85477.1 gg_id:10775 Desulfoarculus sp. str. BG74
EF061952.1 gg_id:182353 Xiamen China mangrove sediment clone XME29
AM882597.1 gg_id:342977 Structure along hydrocarbon contamination coastal sediment oil polluted water pet

DQ330998.1	159453	101.9	342.3	353.8	81.9	134.3	82.3
EF125423.1	184819	706.4	1636.0	875.2	227.0	1257.0	483.8
AY053490.1	39986	3498.9	5208.7	1652.4	929.1	563.8	550.3
AJ620501.1	353759	738.9	1766.1	4217.6	938.2	2005.7	1754.5
FJ746111.1	513493	3820.6	4519.6	6392.2	4366.4	1537.9	3342.2
DQ811817.1	172929	64.2	143.6	79.4	68.0	55.9	20.9
FM242225.1	337177	5845.2	7232.9	7737.4	6013.0	7883.3	6172.6
AB237684.1	139771	150.4	640.9	938.7	154.3	498.1	728.5
AY082461.1	67845	353.1	1491.1	792.8	104.0	227.1	499.7
GU302442.1	552223	2475.1	3383.7	2755.8	2014.0	1919.4	2458.1
AM774314.1	243934	3181.3	3468.1	4787.3	3312.1	4885.1	3073.7
EF999398.1	237632	5659.2	5747.7	9886.6	6084.1	10056.6	6701.0
DQ630706.1	161002	560.2	334.1	832.3	845.6	516.3	847.1
AJ241022.1	10909	21.5	36.0	59.2	56.7	56.8	29.9
DQ831553.1	163459	129.7	488.9	1603.2	340.7	1156.4	522.0
AJ831748.1	102310	71.7	138.1	1927.8	88.9	113.0	64.9
DQ146482.1	164141	1403.0	1435.8	3424.9	950.5	3008.1	1961.1
DQ630702.1	160395	10442.6	12942.0	13592.4	8923.9	10073.9	10470.0
FJ716406.1	571102	5892.3	6608.3	9227.7	4797.6	4654.5	3347.4
AY851291.1	148326	2513.2	3225.5	1922.0	2414.5	3184.1	3456.8
EF688206.1	347101	4368.5	5864.5	6838.9	3254.5	4099.4	4155.1
EU717681.1	425208	5578.8	5373.3	4100.1	3288.4	2011.3	2490.2
U81720.2	10893	35.8	49.9	129.4	54.2	53.4	23.6
GQ356954.1	576546	1308.1	1416.9	1852.5	2348.9	159.5	1286.3
DQ811793.1	173340	2956.8	2634.8	3694.2	2378.9	1669.3	1931.9
AB177130.1	130033	27.6	49.3	29.2	51.5	59.4	22.5
AM774320.1	248513	14201.9	17033.3	13124.6	14045.5	16216.3	12937.0
EU160501.1	325508	1251.6	1842.9	3365.5	2004.4	1688.7	2374.4
U45991.1	10897	20.4	66.5	75.8	53.1	105.5	37.6
EU617853.1	345458	655.3	1425.0	3983.0	614.1	495.6	1232.4
EU246163.1	248972	35.0	70.2	341.0	67.5	100.8	44.8
AM404371.1	558344	6001.9	6585.1	6616.2	5533.0	6832.7	6833.5
AJ620497.1	354146	234.1	329.4	702.6	540.6	461.9	348.3
DQ811815.1	167112	2166.9	2980.3	2430.9	2167.5	1117.1	941.6
DQ811807.1	166757	634.3	1120.7	1626.3	636.4	1296.4	1752.7
DQ397413.1	159387	605.5	780.3	942.6	458.1	1256.5	2005.9
AJ831753.1	106553	346.4	498.1	703.5	397.9	647.7	202.4
DQ004679.1	158084	167.9	127.0	228.4	131.3	61.9	86.8
U85477.1	10775	27.5	50.0	75.4	55.5	98.4	62.4
EF061952.1	182353	897.4	1918.0	2596.7	1020.8	2136.3	1598.3
AM882597.1	342977	5918.1	8026.8	8499.0	5425.0	4849.0	5229.9